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120537

From: Li, Bao-Qun
Sent: Wednesday, April 28, 2004 7:54 AM
To: STIC-Biotech/ChemLib

Please do the sequence homology search for SEQ ID NO: 2 of application SN. 10,089,292. Thanks
Bao Qun Li
Art unit 1648, REM, 3D24.
Tel. 20904

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TECHNICAL INFORMATION
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Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
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Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
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Result No.	Score	Query Match	Length	DB ID	Description
1	1076	98.3	660	1 VHHWH2	structural protein
2	1043	95.3	659	1 AB04212	structural protein
3	91.5	8.4	1305	2 AB0168	probable cell divi
4	91.5	8.4	2130	2 AB0821	probable exported
5	90.5	8.3	261	2 A96484	hypothetical prote
6	90	8.2	1045	2 A39199	endoglucanase B (B
7	89	8.1	291	2 AH3391	biphenyl-1,2,3-diol
8	89	8.1	477	2 C07143	pyruvate kinase (p
9	89	8.1	1802	2 S69703	HKR1 protein precur
10	88.5	8.1	665	2 F95053	cell wall surface
11	88	8.0	583	2 S67571	hypothetical prote
12	87	7.9	329	2 F87318	transcription regu
13	85.5	7.8	817	2 T01866	hypothetical prote
14	85.5	7.8	899	2 T16204	hypothetical prote
15	85	7.8	292	2 AI1937	hypothetical prote
16	84.5	7.7	432	1 AJBCDS	adenylosuccinate s
17	84.5	7.7	432	2 A98273	adenylosuccinate s
18	84.5	7.7	432	2 A86114	adenylosuccinate s
19	84.5	7.7	432	2 AF1049	adenylosuccinate s
20	83.5	7.6	253	2 C75611	transcription regu
21	83	7.6	288	2 T21732	hypothetical prote
22	83	7.6	436	2 T03702	hypothetical prote
23	83	7.6	569	2 C91195	hypothetical prote
24	83	7.6	569	2 DB86042	hypothetical prote
25	83	7.6	617	2 A56051	myocyte nuclear fa
26	83	7.6	765	2 C64981	beta-glucosidase (
27	83	7.6	765	2 C91006	beta-D-glucoside g
28	83	7.6	765	2 DB85850	beta-D-glucoside g
29	83	7.6	2422	2 T12687	ALR protein homolo

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OM Protein - protein search, using sw model

Run on: April 28, 2004, 14:17:48 ; Search time: 20 Seconds (without alignments)

Scoring table: BL2USM22 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Database : PIR_78:*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

VHHWH2

structural protein 2 precursor - hepatitis E virus (strain Burma)

C:Species: hepatitis E virus

C:Accession: C4072A

R:Ram, A.W.; Smith, M.M.; Guerra, M.E.; Huang, C.C.; Bradley, D.W.; Fry, K.E.; Reyes, G.F.; Virology 185, 120-131, 1991

A:Title: Hepatitis E Virus (THEV): molecular cloning and sequencing of the full-length virion genome

A:Reference number: A40778; PMID:92024067; PMID:192677

A:Accession: C40778

A:Molecule type: genomic RNA

A:Residues: 1-660 <TAM>

A:Cross-references: GB:M73218; NID:G330023; PID:AAA45736_1; PMID:g330026

C:Superfamily: hepatitis E virus structural protein 2

C:Keywords: structural protein 2

F:-22/Domain: signal sequence #status Predicted <SIG>

F:23-660/Product: structural protein 2 #status Predicted <SP2>

Query Match %

Best Local Similarity 100.0%; Score 1076; DB 1; Length 660;

Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLFYSPRPVVSANGEPPTVLYTISVNAQQKGIAAPHIDLGESRVITQDYYDNEQDRPT 60

Db 394 QLFYSPRPVVSANGEPPTVLYTISVNAQQKGIAAPHIDLGESRVITQDYYDNEQDRPT 453

QY 61 PSPAPSPRPPSVLRLANDVILMSLTAAEYDOSTYGSSTGPVYVSDSVTLVNATGAQAVARS 120

Db 454 PSPAPSPRPPSVLRLANDVILMSLTAAEYDOSTYGSSTGPVYVSDSVTLVNATGAQAVARS 513

QY 121 LDWTKVTLDGRLPLSTIQVSKTFVFLPLRGKLSFWEAGTIKAGPYNTNTASDOLVEN 180

Db 514 LDWTKVTLDGRLPLSTIQVSKTFVFLPLRGKLSFWEAGTIKAGPYNTNTASDOLVEN 573

QY 181 AAGHRVAISTTYTSLGAGPVSIASAVAVLAP 210

Db 574 AAGHRVAISTTYTSLGAGPVSIASAVAVLAP 603

RESULT 2/

B44212

structural protein 2 precursor - hepatitis E virus (strain Mexico)

C:Species: hepatitis E virus

C:Accession: B44212

R:Huang, C.C.; Nguyen, D.; Fernandez, J.; Yun, K.Y.; Fry, K.E.; Bradley, D.W.; Tam, A.W.; Virology 191, 550-558-1992

A:Title: Molecular Cloning and Sequencing of the Mexico isolate of hepatitis E virus (HEV)

A:Reference number: A44212; PMID:93079857; PMID:1448913

A:Accession: B44212

	Molecule type: genomic RNA
/Residues:	1-659 <HUA>
/Cross-references:	GB: M74506; NID: g310017; PIDN: AAA45732.1; PID: g310020
/Superfamily:	hepatitis B virus structural protein 2
/Keywords:	structural protein
/1-22/Domain:	signal sequence #status predicted <SP1>
/23-659/Product:	structural protein 2 #status predicted <SP2>
Query Match	95.3%; Score 1043; DB 1; Length 659;
Best Local Similarity	94.3%; Pred. No. 3.66-82;
Matches	198; Conservative 9; Missmatches 3; Indels 0; Gaps 0;
y	1 QLFYSPRPVVSANGEPTVKLYTSVNAQODRGIAIPHDIDLGEVRVTDYDQHEDQDRPT 60
o	393 QLFYSPRPVVSANGEPTVKLYTSVNAQODRGIAIPHDIDLGEVRVTDYDQHEDQDRPT 452
b	61 PSPASPRSPFSLVRANDVILWLSLTAAEYDOSTYGSSTGPVYVSDSVTLYNVATGQAAYARS 120
b	453 PSPASPRSPFSLVRANDVILWLSLTAAEYDOSTYGSSTGPVYVSDSVTLYNVATGQAAYARS 512
y	121 LDWTKVTLGRPLSTIQYSKTFPVLPRLGKLSEWAGTTKAGYPNNNTTASDQLLVEN 180
b	513 LDWSKVTLGRPLPVEQFSKTFPVLPRLGKLSEWAGTTKAGYPNNNTTASDQLIJEN 572
y	181 AAGHRAVAISTTYTSAGGPYSISAVAVLAP 210
b	573 AAGHRAVAISTTYTRIGAGPVAISAAVLAP 602
RESULT 3	
B0166	probable cell division protein ftsK [imported] - <i>Yersinia pestis</i> (strain CO92)
/Species:	<i>Yersinia pestis</i>
/Date:	02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
/Accession:	AB0166
/Paratypic:	Paratypic
/Paratype:	J. Wran, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
/Isolate:	eno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Dougan, G.;
/Strain:	1, M.; Fotherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
/Mature:	413, 523-527, 2001
/Title:	Genome sequence of <i>Yersinia pestis</i> , the causative agent of plague.
/Reference:	AB0001; PMID: 1158360
/Accession:	AB0168
/Status:	Preliminary
/Molecule:	genomic DNA
/Residues:	1-1305 <KUR>
/Cross-references:	GB: AL590842; PIDN: CAC90205.1; PID: g15979425; GSPDB: GN00175
/Genetic:	
	;Gene: ftsK
Query Match	8.4%; Score 91.5%; DB 2; Length 1305;
Best Local Similarity	27.9%; Pred. No. 15;
Matches	38; Conservative 17; Missmatches 40; Indels 41; Gaps 7;
y	14 EPTVLYTSVNAQODRGIAIPHDIDLGEVRVTDYDQHEDQDRPTSP----- 63
b	664 EPLFTISPVDETDPEVQE----GREBSLLQDPHQ----VPTYOPPVQOAHLGQS 714
y	64 APSRSPFSLVRANDVILWLSLTAAEYDOSTYGSST---GPVYVSDSVTLYNVATGQAAYAR 119
b	715 APTQP-----SHTQSTYEQSRTGQSTRGQSTPAPVSP-----VVTISASATST 757
y	120 SLDWTKV-TLDGRPLS 134
b	758 SVTPSISASLNTAppS 773
RESULT 4	
B0821	probable exported protein STR2760 [imported] - <i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi
/Species:	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Typhi
/Note:	this species has also been called <i>Salmonella typhi</i>
/Date:	09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
/Accession:	AB0821

R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T. Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
 A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Shelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar Braenderup. A; Reference number: AB0502; MUID:21534947; PMID:11677608
 A; Accession: AB05021
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-2130 <PAR>
 A; Cross-references: GB:AU1513382; PIDN:CAD02718.1; PID:916503731; GSPDB:GN00176
 C; Genetics:
 A; Gene: STY2760

Page 3

RESULT 8							
C70143		pyruvate kinase (pyk) homolog - Lyme disease spirochete					
Qy	57	DRDTPSPAPSRPSVSLRNDVLWLSTAABYDQSTYGSSTGPVYVSDSVTLVNVA-TGAQ	115				
Db	16	DEALPSAAPV-PFAMTPVVRIGKARDAEMLA-----EYYRDVVGIREMARGAS	67				
Qy	116	AVARSLDPTWTKTLDGRPLSTICQYS-----KTFEVLPRLRGKLSFWEAAGTTKA	162				
Db	68	TVLGAGD-----RELMIEEQFSAAARPDPDRSAGLHYTAFLPLPRGDLLARWS-----	113				
Qy	163	GPPYNNTTASQDLINEAAGHRVAASTYTISLGAAGPVNSIA	204				
Db	114	-----RAIDQKPVSGAADHKVSSEAYLTDPPEGNGIEIYVA	149				
RESULT 9							
C70143		Borrelia burgdorferi (Lyme disease spirochete)					
C:Species:		Borrelia burgdorferi (Lyme disease spirochete)					
C:Date:	13-Feb-1998	#Sequence_revision 13-Feb-1998 #text_change 18-Jun-1999					
C:Accession:	C70143						
Qy	8	VIVANGCEPTVKLYTSVEN-----AQDKGIAAP-HDDLGGERV--	45				
Db	200	ILTASGNPDVVKLISKINQEIDNIBIAKASYGTMVARGDMGVETPAEDVPIAQKIKTQ	259				
Qy	46	-----VIQDYNQH---EODRTPSPAPSRRPSVFLRNDVLWLSSLTAEYDQSTYGS	94				
Db	260	TC1JKYGFIVITQMMLTMIENPRTRAESDIANILNGTDAIMLS-----GETAYGK	313				
Qy	95	STGPVYVSDSTVLVNVAQAVARSIDWT-----KVTLDRGPRLSTI	136				
Db	314	-----YPIEAVRM--WTSIAKKVEKRMTHLYKDELFYDKSITRNYIIKCAIDATLMDI	366				
Qy	137	QQYSKTFVLPRLRGKLSFWEAAGTTKAQYPYNNNTTASQDLYENAGHHRV	186				
Db	367	-----KAIIVDSLKGKTARIMA-TYRASVPL-FITINSERLARELAISYGV	410				
RESULT 9							
S69703		protein precursor - yeast (Saccharomyces cerevisiae)					
N:Alternative names:		protein YDR420w					
C:Species:		Saccharomyces cerevisiae					
C:Accession:	S69703	#Sequence_revision 06-Sep-1996 #text_change 23-Mar-2001					
R:Dietrich, F.S.		submitted to the EMBL Data Library, August 1995					
A:Description:	The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831,						
A:Reference number:	S69555						
A:Accession:	S69703						
A:Molecule type:	DNA						
A:Residues:	1-1802 <DNE>						

AA; Cross-references: EMBL:U33007; NID:9927685; PIDN:ABB64857.1; PID:9927691; MIPS:YDR220W
 AA; Residues: 1-581-'A', 583-593-'A', 595-1802 <KAS>
 AA; Cross-references: EMBL:S69101; NID:9545659; PIDN:AAB30051.1; PID:9545660
 AA; Experimental source: YNN235
 AA; Title: Cloning of the *Saccharomyces cerevisiae* gene whose overexpression overcomes the
 C; Genetics:
 AA; Gene: SGD:HKR1
 AA; Cross-references: SGD:S0002828; PMID:8113191
 AA; Accession: A53392
 AA; Molecule type: DNA
 AA; Map position: 4R
 AA; Map keywords: calcium binding; glycoprotein; transmembrane protein
 AA; Status: signal sequence predicted <SIG>
 FF:122-1802/Product: HKRL Protein #status predicted <WAT>
 FF:1483-1508/Domain: transmembrane #status predicted <TMM>
 FF:1645-1656/Domain: calcium binding #status predicted <CAL>
 Query Match Score 89; DB 2; Length 1802;
 Best Local Similarity 26.3%; Pred. No. 38;
 Matches 44; Conservative 24; Mismatches 47; Indels 52; Gaps 8;
 Qy 60 TPSPAPSRRPSVLLRNDVMLSLITAAEYDOSTGGSSTGPVYVSSVTLVNVATGQAQAVAR 119
 Db 1200 TPYPSP-----NSYWLP-PAIVVESSETGPTTASFNPSITGSLPNATEPVAYSE 124.9
 Qy 120 SLDNTKVT-----LDGRPLSTIQGQSKTFVLLRKGKSFWEAGTTKAGYPNNY 168
 Db 1250 PINHNLITIGCTTAIANTYFLVQNPLSSAQ---IENFELPLVK-----YPP 129.1
 Qy 169 NTTASDQLLVENAGHRVALAATSTYLTSLGAG-----PVSIASAVVL 208
 Db 1292 SNTSS---LDDNSGE--LSTFLSYRSRSESSSTLSPKSISSSVV 1332
 Qy 170
 Db 171
 RESULT 10
 F95053 Cell wall surface anchor family protein [imported] - *Streptococcus pneumoniae* (strain T1)
 C;Species: *Streptococcus pneumoniae*
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C;Accession: F95053
 R;Teitelbaum, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidorn, J.D.; Umayam, L.A.; Holt, I.E.; Holt, T.E.; Holtzapple, D.; Radune, M.R.; Lewis, S.L.; Morrison, B.A.; Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Doughterty, B.A.; Morrison, A.; Accession: F95053
 AA; Status: preliminary
 AA; Molecule type: DNA
 AA; Residues: 1-65 <KUR>
 AA; Cross-references: GB:AE005672; PIDN:AAK74623.1; PID:914971934; GSPDB:GN00164; TIGR:SPAC4
 AA; Experimental source: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
 C; Genetics:
 AA; Reference number: A95000; MUID:21357209; PMID:11463916
 AA; Accession: SP0463
 Query Match Score 8.1%; DB 2; Length 665;
 Best Local Similarity 26.9%; Pred. No. 11;
 Matches 42; Conservative 26; Mismatches 51; Indels 37; Gaps 9;
 Qy 12 NGEPTVRL-YTSVNEAQDKGIAIPHDIDGESRVTIQQDYNQHQDRTPSPAPSRRPS 70
 Db 293 NAERKTKYITSAENLYDQSTGGSSTG---VEPVSDSVTLVNVATG-NQAVARSLLDWTK - 339
 Qy 71 VLRANDVMLSLITAAEYDQSTGGSSTG---PVYVSDSVTLVNVATG--AQAVARSLLDWTK 125
 Db 340 ---NEENGDLTLL-----KTVWDAGAP1PAGAEATFDLVNAQTGKVQTVLTDKNT 389
 Qy 126 UTMVDCBPIST-----TOOYSKTPEYLPTLKCKS 154

Db	390	VTVNGLDKNTIEYKFVERSIKGSYADYQETTAGEIA	425
RESULT 11			
S67571	hypothetical protein YDI038C - yeast (Saccharomyces cerevisiae)		
N;Alternate names:	hypothetical protein D2726		
C;Species:	Saccharomyces cerevisiae		
C;Date:	12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002		
C;Accession:	S67571		
R;Paulin, L.; Saren, A.M.; Laamanen, P.	Submitted to the Protein Sequence Database, July 1996		
A;Reference number:	S67560		
A;Accession:	867571		
A;Molecule type:	DNA		
A;Residues:	1-383 <PAU>		
A;Cross-references:	EMBL:Z74087; NID:gi1431021; PID:e252991; PID:gi1431023; GSPDB: A/Gene: MIPS:YDI038C		
A;Cross-references:	SGD:SG0002196		
A;Map position:	4L		
C;Superfamily:	pig submaxillary mucin		
Query Match	8.0%	Score 88; DB 2; Length 583;	
Best Local Similarity	21.8%	Pred. No. 10;	
Matches	48;	Conservative 42; Mismatches 98;	
Indels	32;	Gaps 8;	
Qy	5	SRPVVSRANGEPIVKLYNTSVE-NAQQDQKGIAIPHIDLGESRVVIQDYDNQHEODRPTPSP	63
Db	316	SSVVSSSTSSSEPTSFIVSTSVTSPRSPEPTSTDLATFSDTIILRVSTTSQDQTQVSS	375
Qy	64	AFSPRFPEFLVRDLVWLSLAEYDQSTGPGVTTGSSSTGPVTVYSDSVTLVNVATGAQAVARSLDW	123
Db	376	SLTDMVSSTGSDALSVSSIIQRSDVPSTFAVNSNPVYPTASTG--STSTGPIPTASESSL	433
Qy	124	TK-----VTDLGRLPLSTIQSYKSTFVFLP-----LRQLLSFWEA-GTT	160
Db	434	SRQQGISATSSSSIVLTPVDSASSRSATSIIKPNMPVSSNDSKTQSSVSVDAFQST	493
Qy	161	KAGYP----YNNNTTASDQLVYENAGHRVAIS-TYTTs	194
Db	494	KSSYPSITSADPTTAAENGLYQSSSSAHPITLDRTYASA	533
RESULT 12			
F87318	transcription regulator, probable [imported] - Caulobacter crescentus		
C;Species:	Caulobacter crescentus		
C;Date:	20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 28-Jul-2003		
R;Niezman, W.C.; Felblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haff, D.R.; Hedges, R.J.; Ermoljeva, M.; White, D.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, P.; Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001			
B>Title:	Complete Genome Sequence of Caulobacter crescentus.		
A;Reference number:	A87249; MUID:2117369; PMID:11255647		
A;Accession:	F87318		
A>Status:	Preliminary		
A;Molecule type:	DNA		
A;Residues:	1-329 <STO>		
A;Cross-references:	GB:AE005673; NID:gi13421754; PIDN:AAK22546.1; GSPDB:GN00148		
C;Genetics:			
A;Gene:	CC0560		
C;Superfamily:	Fe2+-dicitrate sensor, transmembrane component		
Query Match	7.9%	Score 87; DB 2; Length 329;	
Best Local Similarity	21.7%	Pred. No. 6.1;	
Matches	54;	Conservative 35; Mismatches 104;	
Indels	56;	Gaps 9;	
Qy	11	ANGEPVTKLVLYTSEVNAQQDKKGIAIPHIDLGESRVVIQDYDNQHEODRPTPSPAPSRRPFS	70

5 AQQGMWVRAVTTSFRTRSPRPRIAPSDLAAASSLV----ESWAEEAGRVTPTVAQRPD5 59
 Db 71 VLRANDVLWISLTAEYDOSTYGS----TGPYYVSDSSV 105
 Qy 60 AERETEAIVDALGA--LDAEDFGSAPAPLWRREVOQGGFTALAAGLAAVWLHGCG 117
 Db 106 TLYNVTGAA---QAYARSLDWTKVTLGRPLRGTLSFW---- 155
 Qy 178 PFTIDAGARAKIVCTQFNVRKT-SDOTRVLLEGHVEYRGRDAEQTLRGAGOAVTVSA 236
 Db 118 DVEPATGAGERVALKDGSRLEINTRSHLEVIRRSHVRMLGEALFMYAARDPHQ 177
 Qy 203 SAVAVLAPP 211
 Db 237 SGATLVRQP 245

RESULT 13
 T01866 hypothetical protein T24M8.3 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
 R;Latreille, P.; Elliott, G.; Le, T.
 submitted to the EMBL Data Library, August 1998
 A;Description: The sequence of A. thaliana T24M8.
 A;Reference number: Z14449
 A;Accession: 101866
 A;Status: translatable from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-817 <LAT>
 A;Cross-references: EMBL:AF07740; PID:93319365
 A;Experimental source: cultivar Columbia
 C;Genetics:
 A;Map position: 4
 A;Introns: 117/3; 188/2; 269/3; 307/3; 357/3; 422/3; 447/1; 486/3; 513/3; 541/3;
 A;Note: T24M8_3

Query Match 7.8%; Score 85.5; DB 2; Length 817;
 Best Local Similarity 22.7%; Pred. No. 27; Mismatches 71; Indels 43; Gaps 9;

Db 516 VIYSHPIHDTSKPKQLESSPPTPEDIQTSQDIG----AHLDENQBSGGYDVDSSPA 572
 Qy 54 HEQDRPTPSAPSRSRFPSVRLRNDVLSLTAAEYD----OSTYGSTGPVY 100
 Db 573 REPERPLSRA----EVFLVAELLSKSCKTGs-YELLPSMSKSFEPALFRNTLSRAPNTEH 626
 Qy 101 VDSVTLYNVTGAAVARSLLDTMK----VTLDRGRPLSTICQYSKTFHFVLP----L 148
 Db 627 LTSSSYLISNKFLISLAKETNNVYSTLIMEVLYSLLSOKLATTLTNQRAAFVQFWFANHL 685
 Qy 149 RGKLSFWBACTTKA 162
 Db 686 QGKLKSFKAAMKMS 699

RESULT 14
 T16204 hypothetical protein F28F5.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
 R;Pauley, A.
 submitted to the EMBL Data Library, April 1994
 A;Description: The sequence of C. elegans cosmid F28F5.
 A;Reference number: Z10477
 A;Accession: T16204
 A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
 A;Residues: 1-899 <PAU>
 A;Cross-references: EMBL:U00045; NID:9470353; PID:9470357; PID:AAA50684.1; CBSP:F28F5.3
 C;Experimental source: strain Bristol N2
 C;Genetics:
 A;Gene: CBSP:F28F5.3
 A;Introns: 22/3; 41/3; 54/3; 72/2; 129/3; 182/3; 307/3; 365/1; 444/3; 525/3; 632/3; 674/1
 C;Superfamily: Caenorhabditis elegans hypothetical protein F28F5.3
 Query Match 7.8%; Score 85.5; DB 2; Length 899;
 Best Local Similarity 24.4%; Pred. No. 30; Mismatches 41; Conservative 20; Indels 53; Gaps 7;
 Matches 41; Score 85.5; DB 2; Length 899;
 Qy 7 PVVVSANGEPPTVK----LYTSVNAQQDKGIAIPHDIDLGESRV----- 45
 Db 457 PVMSARVEATFKQPPREGVKPFVSRQAOD----ITHN--GESKEVNIDLTIILNREQK 509
 Qy 46 -----VIQDYNQHEODRPTPSAPAPRPFSTYLR--ANDVNLMSLTAAEYDQ 89
 Db 510 ATVTPATKYPRTDPLIMDY--HRPQTQILLAPAKPKNSNTRIYHAVIDPFDESPASYYPK 566
 Qy 90 STYG----SSTOPPVYVSDSVTLYNVTGAAVARSLLDTMKYTLGCR 131
 Db 567 QNNGYQRQRRYSSASSASKDGMFTLNVIMGSQPVHGMGFSTVQRDER 614

RESULT 15
 A11937 hypothetical protein alr1052 [Imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AI1937
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuguchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.; DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120
 A;Reference number: AB1807; PMID:21595285; PMID:11759840
 A;Note: A11937
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-292 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA873009.1; PID:917130398; GSDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:

Query Match 7.8%; Score 85.5; DB 2; Length 292;
 Best Local Similarity 25.5%; Pred. No. 7.7; Mismatches 18; Indels 52; Gaps 7;
 Matches 42; Conservative 20; Score 85.5; DB 2; Length 292;

Db 44 RVVQDYNQHEODRPTPEA-----PSRPPSVLRLNDVLSLTAAEYDQ 90
 Qy 134 KLITQSLANKQDSSTTTPKQANSPLITYPAQQTPTDPLPSTIVSDSENSTSSTADVGDS 193
 Db 91 TYGSSTPGVVSDSVTLYNVTGAAVARSLLDTMKYTLGRLPLSTIQYSKTFPVY 145
 Qy 194 ---STTP-----SATLGENNNSAVVTELOGNSWQVTAQD-----KTEFVY 235
 Db 146 LPLRGKLSFWBACTTKA-----TARKQQLTWSGNGAVLV 189
 Db 236 GELTKGDRRTW-----TARKQQLTWSGNGAVLV 265

Search completed: April 28, 2004, 14:21:53
 Job time : 21 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

QY	121	LDWTKVTLDRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGYPYNNNTASDQLIVEN	180	RX MEDLINE=20271579; PubMed=10813471;
Db	198	LDWTKVTLDRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGYPYNNNTASDQLIVEN	257	RA van Cuyck-Gaudre H., Zhang H.Y., Tsarev S.A., Warren R.L., Caudill J.D., Snellings N.J., Begot L., Innis B.I., Longer C.F.; RT "Phylogenetically distinct hepatitis E viruses in Pakistan.";
QY	181	AAGHVAISYTTSLGAGPVSISAVAVLAP	210	RL Am. J. Trop. Med. Hyg. 62:187-189(2000).
Db	258	AAGHVAISYTTSLGAGPVSISAVAVLAP	287	DR EMBL; AFI185822; AAG16766.1; -
				DR GO:0005198; P:structural molecule activity; IEA.
				DR InterPro; IPR004261; SP2.
				DR InterPro; IPR008975; Viral_cap_coat.
				DR Pfam; PF03014; SP2; 1.
				SQ SEQUENCE 660 AA; 70903 MW; 1P506B3CFB3BACCE CRC64;
RESULT 2				
ID Q9YWLO		PRELIMINARY;	PRT;	605 AA.
AC Q9YWLO_1;				
DT 01-MAY-1999 (TREMBIrel. 10, Created)				
DT 01-MAY-1999 (TREMBIrel. 10, Last sequence update)				
DT 01-OCT-2003 (TREMBIrel. 25, Last annotation update)				
DE Structural protein (Fragment).				
OS Hepatitis E virus.				
OC Viruses; ssRNA positive-strand viruses, no DNA stage;				
OX NCBI_TaxID=12461;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=BNC;				
MEDLINE=99013657; PubMed=979311;				
RA Pina S., Jofre J., Emerson S.U., Purcell J.R.H., Girones R.;				
RT "Characterization of a strain of infectious hepatitis E virus isolated from sewage in an area where hepatitis E is not endemic.";				
RT Appl. Environ. Microbiol. 64:4485-4488 (1998).				
DR EMBL; AF058684; AAC77805.1; -				
DR GO:0005198; P:structural molecule activity; IEA.				
DR InterPro; IPR004261; SP2.				
DR InterPro; IPR008975; Viral_cap_coat.				
DR Pfam; PF03014; SP2; 1.				
FT NON_TER	605	605 MW;	A088F76F874B2B72	CRC64;
SQ SEQUENCE 605 AA;	64740	MW;		
Query Match 98.3%; Score 1076; DB 12; Length 605;				
Best Local Similarity 100.0%; Pred. No. 2..e-89;				
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY 1 QLFYSRPVISANGEPVTLYTSVNAQDGKTAIPHDIDGESRVVIDQYDNHEQDDEPT 60				
Db 394 QLFYSRPVISANGEPVTLYTSVNAQDGKTAIPHDIDGESRVVIDQYDNHEQDDEPT 453				
RESULT 4				
Q9WTW9			PRELIMINARY;	PRT;
ID Q9WTW9				660 AA.
AC Q9WTW9_1;				
DT 01-NOV-1999 (TREMBIrel. 12, Created)				
DT 01-NOV-1999 (TREMBIrel. 12, Last sequence update)				
Db 514 LDWTKVTLDRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGYPYNNNTASDQLIVEN 180				
Db 514 LDWTKVTLDRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGYPYNNNTASDQLIVEN 573				
QY 181 AAGHVAISYTTSLGAGPVSISAVAVLAP 210				
Db 574 AAGHVAISYTTSLGAGPVSISAVAVLAP 603				
RP SEQUENCE FROM N.A.				
RC STRAIN=N.A.				
RA 99107414; PubMed=9892396;				
RA Meng J., Cong M., Dai X., Pilott J., Purdy M.A., Fields H.A., Khudyakov Y.E.;				
RA "Primary structure of open reading frame 2 and 3 of the hepatitis E virus isolated from Morocco.";				
RA RL J. Med. Virol. 57:126-133 (1999). [2]				
RN RN SEQUENCE FROM N.A.				
RC STRAIN=Morocco;				
RA Chen G., Meng J.;				
RT "Identification of the 5' Capped and 3' Complete Terminal Sequence of the Hepatitis B virus Isolated From Morocco.";				
RT Submitted (PEB-2003) to the EMBL/GenBank/DDBJ databases.				
RL DR EMBL; AF065061; AAC10527.1; -				
DR GO:0005198; P:structural molecule activity; IEA.				
DR InterPro; IPR004161; SP2.				
DR InterPro; IPR008915; Viral_cap_coat.				
DR Pfam; PF03014; SP2; 1.				
SQ SEQUENCE 660 AA; 70943 MW; 9719D30CCD932950 CRC64;				
RESULT 3				
Q9E8G5		PRELIMINARY;	PRT;	660 AA.
ID Q9E8G5_1;				
AC Q9E8G5_2;				
DT 01-MAR-2001 (TREMBIrel. 16, Created)				
DT 01-OCT-2003 (TREMBIrel. 16, Last sequence update)				
DE Structural protein.				
OS Hepatitis E virus.				
OC Viruses; ssRNA positive-strand viruses, no DNA stage;				
OC Hepatitis E-like viruses.				
OX NCBI_TaxID=12461;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=Abb-2B;				

Qy	1	QLFYSPRPVVAANGEPTVKLYTSVENAQODKGIAIPHIDIGESRVVIQDYDNQHQEQRPT	60	DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
Db	394	QLFYSRPPVVAANGEPTVKLYTSVENAQODKGIAIPHIDIGESRVVIQDYDNQHQEQRPT	453	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db	61	PSPAPSRPFPVLRANDVLWLSLTAAEYDOSTYGSSTGPyVSDSVTLVNVATGQAQAVARS	120	DB	Structural protein.
Qy	454	PSPAPSRPFPVLRANDVLWLSLTAAEYDOSTYGSSTGPyVSDSVTLVNVATGQAQAVARS	513	OS	Hepatitis E virus.
Db	121	LDTWTKVTLDRPLSTIQSKTFFVPLRGKLSFWEAGTAKAGPYNNNTTASDQLVEN	180	OC	ssRNA positive-strand viruses, no DNA stage;
Db	514	LDTWTKVTLDRPLSTIQSKTFFVPLRGKLSFWEAGTAKAGPYNNNTTASDQLVEN	573	OC	Hepatitis E-like viruses.
Qy	181	AAGHRAVIASTYTTSISLGAGPVSIASAVAVLP	210	NCBI_TaxID=12461;	[1]
Db	574	AAGHRAVIASTYTTSISLGAGPVSIASAVAVLP	603	RN	SEQUENCE FROM N.A.
RESULT 5				RP	
Q8J732		:PRELIMINARY;	PRT;	RC	STRAIN=Rev037;
ID	Q8J732			RA	Donati M.C., Pagan E.A., Harrison T.J.;
AC	Q8J732;			RL	"Sequence analysis of full length HEV clones derived directly from
DT	01-OCT-2002 (TREMBLrel. 22, Created)			RR	human liver in fulminant hepatitis E."
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			GO; GO:0005138; F	structural molecule activity; IEA.
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			InterPro; IPR004261; SP2.	
DE	Capsid Protein.			InterPro; IPR008975; Viral_cap_coat.	
OS	Hepatitis E virus.			Pfam; PF03014; SP2;	
OC	ssRNA positive-strand viruses, no DNA stage;			SEQUENCE 660 AA; F37E3FERF7A4BAD1 CRC64;	
OC	Hepatitis E-like viruses.			Query Match 97.9%; Score 1072; DB 12; Length 660;	
RN	NCBI_TaxID=12461;			Best Local Similarity 99.0%; Pred. No. 6.3e-89; Mismatches 0; Indels 0; Gaps 0;	
[1]				RR	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RP	SEQUENCE FROM N.A.			RR	EMBL; X88292; CAA65937.1;
RX	MEDLINE=200202932; PubMed=12076829;			DR	GO; GO:0005138; F
RA	Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;			DR	structural molecule activity; IEA.
RT	"Reanalysis of a North India isolate of hepatitis E virus based on			DR	InterPro; IPR004261; SP2.
RT	the full-length genomic sequence obtained following long RT-PCR."			DR	InterPro; IPR008975; Viral_cap_coat.
RL	Virus Res. 86:53-58 (2002).			Pfam; PF03014; SP2;	
RN	SEQUENCE FROM N.A.			SEQUENCE 660 AA; F37E3FERF7A4BAD1 CRC64;	
RA	Jameel S., Zafrullah M., Chawla Y.K., Dilawari J.B.;			Query Match 97.9%; Score 1072; DB 12; Length 659;	
RA	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			Best Local Similarity 99.5%; Pred. No. 6.3e-89; Mismatches 0; Indels 0; Gaps 0;	
DR	EMBL; AF059438; AAC66330.1; -			RR	PRELIMINARY; PRT; 660 AA.
DR	GO; GO:0005138; F			AC	Q89468 PRELIMINARY; PRT; 660 AA.
DR	InterPro; IPR004261; SP2.			AC	Q89468; 01-NOV-1996 (TREMBLrel. 01, Created)
DR	InterPro; IPR008975; Viral_cap_coat.			DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DR	Pfam; PF03014; SP2;			DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
SQ	SEQUENCE 659 AA; 70842 MW;	ABC177BEBE6012C8 CRC64;		DB	UNNAMED Protein product.
Query Match 97.9%; Score 1072; DB 12; Length 659;				OS	Hepatitis E virus.
Best Local Similarity 99.5%; Pred. No. 6.3e-89; Mismatches 0; Indels 0; Gaps 0;				OC	ssRNA positive-strand viruses, no DNA stage;
Matches 209; Conservative 0; Mismatches 0;				OC	Hepatitis E-like viruses.
RESULT 7				NCBI_TaxID=12461;	[1]
Qy	1	QLFYSPRPVVAANGEPTVKLYTSVENAQODKGIAIPHIDIGESRVVIQDYDNQHQEQRPT	60	RN	SEQUENCE FROM N.A.
Db	393	QLFYSRPPVVAANGEPTVKLYTSVENAQODKGIAIPHIDIGESRVVIQDYDNQHQEQRPT	452	RP	SEQUENCE FROM N.A.
Qy	61	PSPAPSRPFPVLRANDVLWLSLTAAEYDOSTYGSSTGPyVSDSVTLVNVATGQAQAVARS	120	RC	STRAIN=F52-87;
Db	453	PSPAPSRPFPVLRANDVLWLSLTAAEYDOSTYGSSTGPyVSDSVTLVNVATGQAQAVARS	512	RX	Medline=7871757;
Qy	121	LDTWTKVTLDRPLSTIQSKTFFVPLRGKLSFWEAGTAKAGPYNNNTTASDQLVEN	180	RA	Yin S., Purcell R.H., Emerson S.U.;
Db	513	LDTWTKVTLDRPLSTIQSKTFFVPLRGKLSFWEAGTAKAGPYNNNTTASDQLVEN	572	RT	"A new Chinese isolate of hepatitis E virus: comparison with strains recovered from different geographical regions.";
Qy	181	AAGHRAVIASTYTTSISLGAGPVSIASAVAVLP	210	RT	Virus Genes 9:23-32(1994).
Db	573	AAGHRAVIASTYTTSISLGAGPVSIASAVAVLP	602	RL	
RESULT 6				RN	
Q69411		:PRELIMINARY;	PRT;	RA	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
ID	Q69411;			RR	[2]
AC	Q69411;			RR	
DT	01-NOV-1996 (TREMBLrel. 01, Created)			RR	

DR	EMBL; L25547; AAA91080_1; -.	Qy	181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210
DR	EMBL; L25549; AA65649_1; -.	Db	574 AAGHRVAISTYTTSLGAGPVSISAVAVFAP 603
DR	GO:0005199; P:structural molecule activity; IEA.		
DR	InterPro; IPR004261; SP2.		
DR	InterPro; IPR008975; Viral_cap_coat.		
DR	Pfam; PF03014; SP2; 1.		
SEQUENCE	660 AA; 70979 MW; DC68116DCD639175, CRC64;		
Query Match	97.9%; Score 1072; DB 12; Length 660;		
Best Local Similarity	99.5%; Pred. No. 6.3e-89;		
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1 QLFYSPRPVVSANGPPTVKLYTSVENAQQDKGIAIPHDIDGESRVVQDYDNQHEQDRT 60		
Db	394 QLFYSPRPVVSANGPPTVKLYTSVENAQQDKGIAIPHDIDGESRVVQDYDNQHEQDRT 453		
Qy	61 PSPAPSRPFPSVLRANDVLWSLTAAEYDOSTSSTGPVYVSDSVTLVNVATAQAVARS 120		
Db	454 PSPAPSRPFPSVLRANDVLWSLTAAEYDOSTSSTGPVYVSDSVTLVNVATAQAVARS 513		
Qy	121 LDWTKVTLGRPLSTIQSKTFFVLPRLRGKLSFWEAGTTKAGXPNTNTASDOLIVEN 180		
Db	514 LDWTKVTLGRPLSTIQSKTFFVLPRLRGKLSFWEAGTTKAGXPNTNTASDOLIVEN 573		
Qy	181 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 210		
Db	574 AAGHRVAISTYTTSLGAGPVSISAVAVLAP 603		
RESULT 8			
Q9NQAO	PRELIMINARY; PRT; 660 AA.		
ID	Q9NQAO; PRELIMINARY; PRT; 660 AA.		
AC	O9NQAO; PRELIMINARY; PRT; 660 AA.		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	ORF 2.		
DE	Repetitive E virus.		
OS	Viruses; ssRNA positive-strand viruses, no DNA stage;		
OC	Hepatitis E-like viruses.		
OX	Arankalle V.A.; Patanjape S., Emerson S.U., Purcell R.H., Walimbe A.M.;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ANL-90; PubMed=10423137;		
RC	RA: GO:0005000; PubMed=10423137;		
RC	RA: Arankalle V.A., Patanjape S., Emerson S.U., Purcell R.H., Walimbe A.M.;		
RT	"Phylogenetic analysis of hepatitis E virus isolates from India (1976-1993);";		
RT	J. Gen. Virol. 80:1691-1700(1999).		
RL	EMBL; AF24407; AAC05493.1; -.		
DR	GO:0005198; P:structural molecule activity; IEA.		
DR	InterPro; IPR004261; SP2.		
DR	InterPro; IPR008975; Viral_cap_coat.		
SEQUENCE	660 AA; 71041 MW; 03B72DDFOAB7B521, CRC64;		
Query Match	97.9%; Score 1072; DB 12; Length 660;		
Best Local Similarity	99.5%; Pred. No. 6.3e-89;		
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy	1 QLFYSPRPVVSANGPPTVKLYTSVENAQQDKGIAIPHDIDGESRVVQDYDNQHEQDRT 60		
Db	394 QLFYSPRPVVSANGPPTVKLYTSVENAQQDKGIAIPHDIDGESRVVQDYDNQHEQDRT 453		
Qy	61 PSPAPSRPFPSVLRANDVLWSLTAAEYDOSTSSTGPVYVSDSVTLVNVATAQAVARS 120		
Db	454 PSPAPSRPFPSVLRANDVLWSLTAAEYDOSTSSTGPVYVSDSVTLVNVATAQAVARS 513		
Qy	121 LDWTKVTLGRPLSTIQSKTFFVLPRLRGKLSFWEAGTTKAGXPNTNTASDOLIVEN 180		
Db	514 LDWTKVTLGRPLSTIQSKTFFVLPRLRGKLSFWEAGTTKAGXPNTNTASDOLIVEN 573		
RESULT 9			
Q9NQAO	PRELIMINARY; PRT; 660 AA.		
ID	Q9NQAO; PRELIMINARY; PRT; 660 AA.		
AC	O9NQAO; PRELIMINARY; PRT; 660 AA.		
DT	01-NOV-1999 (TREMBLrel. 12, Created)		
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	ORF 2.		
DE	Repetitive E virus.		
OS	Viruses; ssRNA positive-strand viruses, no DNA stage;		
OC	Hepatitis E-like viruses.		
OX	Arankalle V.A.; Patanjape S., Emerson S.U., Purcell R.H., Walimbe A.M.;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=99105430; PubMed=9890424;		
RC	RA: Tsare S.A., Benn L.N., Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Innis B.L.;		
RT	"Phylogenetic analysis of hepatitis E virus isolates from Egypt.";		
RL	J. Med. Virol. 57:68-74(1999).		
DR	GO:0005198; P:structural molecule activity; IEA.		
DR	InterPro; IPR004261; SP2.		
DR	InterPro; IPR008975; Viral_cap_coat.		
SEQUENCE	660 AA; 71040 MW; 044FF5EA7C492791, CRC64;		
Query Match	97.9%; Score 1072; DB 12; Length 660;		
Best Local Similarity	99.0%; Pred. No. 6.3e-89;		
Matches 208; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
Qy	1 QLFYSPRPVVSANGPPTVKLYTSVENAQQDKGIAIPHDIDGESRVVQDYDNQHEQDRT 60		
Db	394 QLFYSPRPVVSANGPPTVKLYTSVENAQQDKGIAIPHDIDGESRVVQDYDNQHEQDRT 453		
Qy	61 PSPAPSRPFPSVLRANDVLWSLTAAEYDOSTSSTGPVYVSDSVTLVNVATAQAVARS 120		
Db	454 PSPAPSRPFPSVLRANDVLWSLTAAEYDOSTSSTGPVYVSDSVTLVNVATAQAVARS 513		
Qy	121 LDWTKVTLGRPLSTIQSKTFFVLPRLRGKLSFWEAGTTKAGXPNTNTASDOLIVEN 180		
Db	514 LDWTKVTLGRPLSTIQSKTFFVLPRLRGKLSFWEAGTTKAGXPNTNTASDOLIVEN 573		
RESULT 10			
Q9NQAO	PRELIMINARY; PRT; 660 AA.		
ID	Q9NQAO; PRELIMINARY; PRT; 660 AA.		
AC	O9NQAO; PRELIMINARY; PRT; 660 AA.		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Structural protein.		
DE	Hepatitis E virus.		
OS	Viruses; ssRNA positive-strand viruses, no DNA stage;		
OC	Hepatitis E-like viruses.		
OX	NCBI_TaxID=12461;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=99105430; PubMed=9890424;		
RC	RA: Tsare S.A., Benn L.N., Gomatos P.J., Arthur R.R., Monier M.K., van Cuyck-Gandre H., Longer C.F., Innis B.L.;		
RT	"Phylogenetic analysis of hepatitis E virus isolates from Egypt.";		
RL	J. Med. Virol. 57:68-74(1999).		

Db	394	QLFYSRPVVSANGEPTVKLYTSVENAQDKGIAIPHDIDGESRVVIQDYDNQHEQDRPT 453														
		DT	01-JAN-1998	(TREMBLrel.	05;	Created)										
Qy	61	PSPAPSRRPFSVLRANDVLMISLTAAEYDOSTYGSSTGPVYVSISVTLYVNATGAQAVARS	120	DT	01-JAN-1998	(TREMBLrel.	05;	Last sequence update)								
Db	454	PSPAPSRRPFSVLRANDVLMISLTAAEYDOSTYGSSTGPVYVSISVTLYVNATGAQAVARS	513	DT	01-OCT-2003	(TREMBLrel.	25;	Last annotation update)								
Qy	121	LDWTKVTLDRPLSTIQSKTFVFLPLRGKLSWEAGTTKAGYPNTNTASDQLLVEN 180		DE	Structural protein 2 (Fragment).											
Qy	514	LDWTKVTLDRPLSTIQSKTFVFLPLRGKLSWEAGTTKAGYPNTNTASDQLLVEN 180		OS	Hepatitis E virus.											
Db	514	LDWTKVTLDRPLSTIQSKTFVFLPLRGKLSWEAGTTKAGYPNTNTASDQLLVEN 180		OC	ssRNA positive-strand viruses, no DNA stage;											
Qy	181	AAGHRVAISTYTTSISLGAGPVSISSAVAVLAP 210		OC	Hepatitis E-like viruses.											
Db	574	AAGHRVAISTYTTSISLGAGPVSISSAVAVLAP 603		RN	NCBI_TaxID=12461;											
RESULT 1.3																
Q9WIL4	ID	Q9WIL4	PRELIMINARY;	PRT;	660 AA.	SEQUENCE FROM N.A.										
AC		Q9WIL4;														
DT	01-NOV-1999	(TREMBLrel.	12;	Created)		RC STRAIN=Chad T3;										
DT	01-NOV-1999	(TREMBLrel.	12;	Last sequence update)		RA Van Cuyck-Gandrie H., Caudill J., Clements N., Zhang H., Buisson Y.,										
DT	01-OCT-2003	(TREMBLrel.	25;	Last annotation update)		RA Cohen S., Warren R., Longer C.;										
DE	Capsid protein.															
OS	Hepatitis E virus.															
OC	ssRNA positive-strand viruses, no DNA stage;															
OC	Hepatitis E-like viruses.															
OX	NCBI_TaxID=12461;															
RN	[1]															
RP	SEQUENCE FROM N.A.															
RC	STRAIN=PK15/92;															
RX	MEDLINE=9049628; PubMed=98333882;															
RA	RA Gouvea V., Snellings N., Popok M.J., Longer C.F., Innis B.L.;															
RT	"Hepatitis E virus: complete genome sequence and phylogenetic analysis of a Nepali isolate."															
RT	Virus Res. 57:21-26 (1998).															
RL	[2]															
RN	RP SEQUENCE FROM N.A.															
RC	STRAIN=PK15/92;															
RA	Gouvea V.;															
RL	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.															
DR	EMBL; AF051830; AAC97188.1; -															
GO	GO:0005198; F_structural molecule activity; IEA.															
DR	InterPro IPRO04261; SP2.															
DR	InterPro IPRO08975; Viral_cap_coat.															
DR	PFAM; PF03014; SP2; 1.															
SQ	SEQUENCE 660 AA; 70798 MW; A04C0165ACC085DB CRC64;															
RESULT 13																
Q9WIL4	ID	Q9WIL4	PRELIMINARY;	PRT;	660 AA.	SEQUENCE FROM N.A.										
AC		Q9WIL4;														
DT	01-NOV-1999	(TREMBLrel.	12,	Created)		RA SEQUENCE FROM N.A.										
DT	01-OCT-2003	(TREMBLrel.	25,	Last annotation update)		RA STRAIN=Chad T3;										
DE	Capsid protein.															
OS	Hepatitis E virus.															
OC	ssRNA positive-strand viruses, no DNA stage;															
OC	Hepatitis E-like viruses.															
RN	[1]															
RP	SEQUENCE FROM N.A.															
RC	STRAIN=PK15/92;															
RX	MEDLINE=9049628; PubMed=98333882;															
RA	RA Gouvea V., Snellings N., Popok M.J., Longer C.F., Innis B.L.;															
RT	"Hepatitis E virus: complete genome sequence and phylogenetic analysis of a Nepali isolate."															
RT	Virus Res. 57:21-26 (1998).															
RL	[2]															
RN	RP SEQUENCE FROM N.A.															
RC	STRAIN=PK15/92;															
RA	RA Gouvea V.;															
RT	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.															
DR	EMBL; AF051830; AAC97188.1; -															
GO	GO:0005198; F_structural molecule activity; IEA.															
DR	InterPro IPRO04261; SP2.															
DR	InterPro IPRO08975; Viral_cap_coat.															
DR	PFAM; PF03014; SP2; 1.															
SQ	SEQUENCE 660 AA; 70798 MW; A04C0165ACC085DB CRC64;															
RESULT 13																
Q9WIL4	ID	Q9WIL4	PRELIMINARY;	PRT;	525 AA.	SEQUENCE FROM N.A.										
AC		Q9WIL4;														
DT	01-JAN-1998	(TREMBLrel.	05;	Created)		RA SEQUENCE FROM N.A.										
DT	01-OCT-2003	(TREMBLrel.	25;	Last annotation update)		RA STRAIN=Chad T3;										
DE	Structural protein 2 (Fragment).															
OS	Hepatitis E virus.															
OC	ssRNA positive-strand viruses, no DNA stage;															
OC	Hepatitis E-like viruses.															
RN	[1]															
RP	SEQUENCE FROM N.A.															
RC	STRAIN=PK15/92;															
RX	MEDLINE=9049628; PubMed=98333882;															
RA	RA Gouvea V., Snellings N., Popok M.J., Longer C.F., Innis B.L.;															
RT	"Hepatitis E virus: complete genome sequence and phylogenetic analysis of a Nepali isolate."															
RT	Virus Res. 57:21-26 (1998).															
RL	[2]															
RN																

Qy	1	QLFYSRPVVSANGEPTVKLYT'SVENAQODKGIAIPHIDIGESRVVIQDYDNOHQEQDRPT	60
Db	394	QLFYSRPVVSANGEPTVKLYT'SVENAQODKGIAIPHIDIGESRVVIQDYDNOHQEQDRPT	453
Qy	61	PSPASRPFSTVLRSNLTAAEYDQSTGGSSTGPVYVSDSYTLYNATGQAVERS	120
Db	454	PSPASRPFSTVLRSNLTAAEYDQSTGGSSTGPVYVSDSYTLYNATGQAVERS	513
Qy	121	LDWTKVTLDORPLSTIQSKTFVPLRKLFSWEAGTTKAGPYNTNTTASDOLLVEN	180
Db	514	LDWTKVTLDORPLSTIQSKTFVPLRKLFSWEAGTTKAGPYNTNTTASDOLLVEN	573
Qy	181	AAGHVAISYTTSLGAGPVISAVAVLAP	210
Db	574	AAGHVAISYTTSLGAGPVISAVAVLAP	603

Search completed: April 28, 2004, 14:21:21
 Job time : 47 secs

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OM protein - protein search, using SW model

Run on: April 28, 2004, 14:18:43 ; Search time 22 Seconds
(without alignments)

Title: US-10-089-292A-2

Perfect score: 1095

Sequence: 1 QLFYSPVVSANGEPTPVKLY..... SLGAGPVSISAVAVLAPPR 213

Scoring table: BLOSUM62

Gapcost: 0.5

Searched:

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgnd_6/.ptodata/2/iaa/5A_COMBO.pep.*
 2: /cgnd_6/.ptodata/2/iaa/5B_COMBO.pep.*
 3: /cgnd_6/.ptodata/2/iaa/6A_COMBO.pep.*
 4: /cgnd_6/.ptodata/2/iaa/6B_COMBO.pep.*
 5: /cgnd_6/.ptodata/2/iaa/BCTUS_COMBO.pep.*
 6: /cgnd_6/.ptodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1076	98.3	267	4	US-09-172-699-18
2	1076	98.3	327	1	US-08-240-049B-13
3	1076	98.3	327	1	US-08-259-148A-15
4	1076	98.3	327	1	US-08-484-054-15
5	1076	98.3	327	2	US-08-876-941A-15
6	1076	98.3	327	3	US-08-542-634-17
7	1076	98.3	327	3	US-08-477-292-17
8	1076	98.3	327	4	US-08-870-985A-15
9	1076	98.3	327	5	PCT-US95-13703-17
10	1076	98.3	436	1	US-08-259-148A-17
11	1076	98.3	436	1	US-08-484-054-17
12	1076	98.3	436	2	US-07-876-941A-17
13	1076	98.3	436	4	US-07-870-985A-17
14	1076	98.3	525	3	US-08-542-634-27
15	1076	98.3	525	5	PCT-US95-13703-27
16	1076	98.3	540	3	US-08-542-634-25
17	1076	98.3	540	5	PCT-US95-13703-25
18	1076	98.3	549	3	US-08-542-634-15
19	1076	98.3	549	3	US-08-477-292-15
20	1076	98.3	549	5	PCT-US95-13703-15
21	1076	98.3	552	4	US-09-172-699-20
22	1076	98.3	561	4	US-09-462-606-50
23	1076	98.3	660	1	US-08-240-049B-15
24	1076	98.3	660	1	US-08-259-148A-19
25	1076	98.3	660	1	US-08-484-054-19
26	1076	98.3	660	2	US-07-876-941A-19
27	1076	98.3	660	3	US-08-840-316-2

RESULT 1
US-09-172-699-18

; Sequence 18, Application US/09172699A
; Patent No. 651690 ✓
; GENERAL INFORMATION:
; APPLICANT: Anderson, David A.
; APPLICANT: Locarnini, Stephen A.
; APPLICANT: Toressi, Joseph
; APPLICANT: Hui, Zhuang
; APPLICANT: Li, Fan
; TITLE OF INVENTION: IMMUNOREACTIVE ANTIGENS OF HEPATITIS E VIRUS
; FILE REFERENCE: Davies Col. Cave
; CURRENT APPLICATION NUMBER: US/09/172,699A
; EARLIER APPLICATION NUMBER: 08/1617,927
; EARLIER FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 18
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-172-699-18

Query Match 98.3%; Score 1076; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 3, 2e-104;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLPLYSRPLVVSANGEPTVLYTSTENAAQDKGTAIPIHDGLSERVVDYDNEQDRT 60
Db 1 QLFYSPRPLVVSANGEPTVLYTSTENAAQDKGTAIPIHDGLSERVVDYDNEQDRT 60

Qy 61 PSPAPSRSFSLVRLNDVWLSLTAAYEQDOSTGSSTGPPVYSDSVTLVNVATGAQAVARS 120
Db 61 PSPAPSRSFSLVRLNDVWLSLTAAYEQDOSTGSSTGPPVYSDSVTLVNVATGAQAVARS 120

Qy 121 LDWTKVTDGRPLSTIQSKTFVPLPLRGKLSFWEAGTTKAGPYNNNTASDQLVEN 180
Db 121 LDWTKVTDGRPLSTIQSKTFVPLPLRGKLSFWEAGTTKAGPYNNNTASDQLVEN 180

Qy 181 AAGHRVAISTYTSLGAGPVSISAVAVLAP 210
Db 181 AAGHRVAISTYTSLGAGPVSISAVAVLAP 210

RESULT 2
US-08-240-049B-13
; Sequence 13, Application US/08240049B
; Patent No. 5686339
; GENERAL INFORMATION:
; Sequence 2, Appli

APPLICANT: Reyes, Gregory R.
 APPLICANT: Tam, Albert W.
 APPLICANT: Yarbough, Patrice O.
 TITLE OF INVENTION: Hepatitis E Virus Peptides and Methods
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genelabs Technologies, Inc.
 STREET: 505 Penobscot Drive
 CITY: Redwood City
 STATE: CA
 ZIP: 94063
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,049B
 FILING DATE: 09-MAY-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Charles K. Sholtz
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 4600-0093.35; G32P4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 SEQUENCE CHARACTERISTICS:
 LENGTH: 327 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
 INDIVIDUAL ISOLATE: region
 US-08-240-049B-13

Query Match 98.3%; Score 1076; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.4e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVVSAANGEPTVKLYTSVNAQQDGIAIPHDIDGESRVIQDYYDNQHEQDRPT 60
 Db 61 QLFYSPRVVSAANGEPTVKLYTSVNAQQDGIAIPHDIDGESRVIQDYYDNQHEQDRPT 120
 Qy 61 PSPAPSRRPFLVRANDVILSLTAEYDOSTYGSSTGPVYVSDVTLVNVATGAAQAVARS 120
 Db 121 PSPAPSRRPFLVRANDVILSLTAEYDOSTYGSSTGPVYVSDVTLVNVATGAAQAVARS 180
 Qy 121 LDWTKVTLDRPLSTIQSKTFFVLPLRGKLSWWEAGTTKAGYPNNNTASDQLLVEN 180
 Db 181 LDWTKVTLDRPLSTIQSKTFFVLPLRGKLSWWEAGTTKAGYPNNNTASDQLLVEN 240

Qy 181 AAGHRAVIASTTYTTSLGAGPVSISAVAVLAP 210

Db 241 AAGHRAVIASTTYTTSLGAGPVSISAVAVLAP 270

RESULT 3
 US-08-259-148A-15
 Sequence 15, Application US/08259148A
 Patent No. 574190
 GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R.
 APPLICANT: Bradley, Daniel W.
 APPLICANT: Twu, Jr-shin
 APPLICANT: Purdy, Michael A.
 APPLICANT: Krawczynski, Krzysztof Z.
 APPLICANT: Yarbough, Patrice D.

; TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/259,148A
 ; FILING DATE: 13-JUN-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 822,335
 ; FILING DATE: 17-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 505,888
 ; FILING DATE: 05-APR-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 420,921
 ; FILING DATE: 13-OCT-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 367,486
 ; FILING DATE: 16-JUN-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 336,672
 ; FILING DATE: 11-APR-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 208,997
 ; FILING DATE: 17-JUN-1988
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sholtz, Charles K.
 ; REGISTRATION NUMBER: 38,615
 ; REFERENCE/DOCKET NUMBER: 4600-0093.20
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 327 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
 ; US-08-259-148A-15

Query Match 98.3%; Score 1076; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.4e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVVSAANGEPTVKLYTSVNAQQDGIAIPHDIDGESRVIQDYYDNQHEQDRPT 60
 Db 61 QLFYSPRVVSAANGEPTVKLYTSVNAQQDGIAIPHDIDGESRVIQDYYDNQHEQDRPT 120
 Qy 61 LDWTKVTLDRPLSTIQSKTFFVLPLRGKLSWWEAGTTKAGYPNNNTASDQLLVEN 180
 Db 121 LDWTKVTLDRPLSTIQSKTFFVLPLRGKLSWWEAGTTKAGYPNNNTASDQLLVEN 240

Qy 121 AAGHRAVIASTTYTTSLGAGPVSISAVAVLAP 210

Db 181 AAGHRAVIASTTYTTSLGAGPVSISAVAVLAP 270

Qy 241 AAGHRAVIASTTYTTSLGAGPVSISAVAVLAP 270

RESULT 3
 US-08-259-148A-15
 Sequence 15, Application US/08259148A
 Patent No. 574190
 GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R.
 APPLICANT: Bradley, Daniel W.
 APPLICANT: Twu, Jr-shin
 APPLICANT: Purdy, Michael A.
 APPLICANT: Krawczynski, Krzysztof Z.
 APPLICANT: Yarbough, Patrice D.

RESULT 4
 Sequence 05-15 Application US/08484054
 / Patent No 520689
 / GENERAL INFORMATION:
 / APPLICANT: Reyes, Gregory R.
 / APPLICANT: Bradley, Daniel W.
 / APPLICANT: Twu, Jr-Shin
 / APPLICANT: Purdy, Michael A.
 / APPLICANT: Tam, Albert W.
 / APPLICANT: Kravcynski, Krzysztof Z.
 / TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 / NUMBER OF SEQUENCES: 22
 / ADDRESSEE: Dehlinger & Associates
 / STREET: 350 Cambridge Avenue, Suite 250
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94306
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/484,054
 / FILING DATE: 07-JUN-1995
 / CLASSIFICATION: 424
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 870,985
 / FILING DATE: 20-APRIL-1992
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 822,335
 / FILING DATE: 17-JAN-1992
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 505,888
 / FILING DATE: 05-APRIL-1990
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 420,921
 / FILING DATE: 13-OCTOBER-1989
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 367,486
 / FILING DATE: 16-JUNE-1989
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 336,672
 / FILING DATE: 11-APRIL-1989
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 208,997
 / FILING DATE: 17-JUNE-1988
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Sholtz, Charles K.
 / REGISTRATION NUMBER: 38,615
 / REFERENCE/DOCKET NUMBER: 4600-0093.38
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 324-0880
 / TELEFAX: (415) 324-0960
 / INFORMATION FOR SEQ ID NO: 15:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 327 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ORIGINAL SOURCE:
 / INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
 / US-08-484-054-15

Query Match 98.3%; Score 1076; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.4e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-07-876-941A-15
 ; Sequence 15 Application US/07876941A
 ; Patent No 5885768
 / GENERAL INFORMATION:
 / APPLICANT: Reyes, Gregory R.
 / APPLICANT: Bradley, Daniel W.
 / APPLICANT: Tam, Albert W.
 / APPLICANT: Mitchell, Carl
 / TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
 / NUMBER OF SEQUENCES: 76
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Dehlinger & Associates
 / STREET: 350 Cambridge Avenue, Suite 250
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94306
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent In Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/07/876,941A
 / FILING DATE: 01-MAY-1992
 / CLASSIFICATION: 435
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 822,335
 / FILING DATE: 17-JAN-1992
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 505,888
 / FILING DATE: 05-APRIL-1990
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 420,921
 / FILING DATE: 13-OCTOBER-1989
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 367,486
 / FILING DATE: 16-JUNE-1989
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 336,672
 / FILING DATE: 11-APRIL-1989
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 208,997
 / FILING DATE: 17-JUNE-1988
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Sholtz, Charles K.
 / REGISTRATION NUMBER: 38,615
 / REFERENCE/DOCKET NUMBER: 4600-0093.38
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 324-0880
 / TELEFAX: (415) 324-0960
 / INFORMATION FOR SEQ ID NO: 15:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 327 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ORIGINAL SOURCE:
 / INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
 / US-08-484-054-15

Query Match 98.3%; Score 1076; DB 1; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.4e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LENGTH: 327 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
 US-07-876-941A-15

Query Match 98.3%; Score 1076; DB 2; Length 327;
 Best Local Similarity 100.0%; P-Value: 4.4e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRPVVSANGEPTVKLYTSVENAQDQKGIAIPHDIDGESRVVIQDYDNQHEQDRPT 60
 Db 61 QLFYSPRPVVSANGEPTVKLYTSVENAQDQKGIAIPHDIDGESRVVIQDYDNQHEQDRPT 120
 Qy 61 PSPAPSRPFSVLANDVWLSTAAYEQSTSYSSGPPVSDSVTLYNVAATGAQAVARS 120
 Db 121 PSPAPSRPFSVLANDVWLSTAAYEQSTSYSSGPPVSDSVTLYNVAATGAQAVARS 180
 Qy 121 LDWTKVTLGRPLSTIQSYKSTFVLPURGKLSTAEYDOSTYGSSTGPVYSDSVTLYNVAATGAQAVARS 180
 Db 181 LDWTKVTLGRPLSTIQSYKSTFVLPURGKLSTAEYDOSTYGSSTGPVYSDSVTLYNVAATGAQAVARS 240
 Qy 181 AAGHRVAISTYTTSLGAGPVSI SAVAVLAP 210
 Db 241 AAGHRVAISTYTTSLGAGPVSI SAVAVLAP 270

RESULT 6
 US-08-477-292-1
 Sequence 17, Application US/08477292
 ; Patent No. 6214910
 ; GENERAL INFORMATION:
 ; APPLICANT: Fuerst, Thomas R.
 ; APPLICANT: McAtee, Patrick C.
 ; APPLICANT: Yarbrough, Patrice O.
 ; APPLICANT: Zhang, Yifan
 ; TITLE OF INVENTION: Hepatitis E Virus Antigens and Methods
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cathleen M. Desjardins, M.D.
 ; STREET: 505 Penobscot Drive
 ; CITY: Redwood City
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94063
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,292
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, Allan A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: G32PS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 369-9500
 ; TELEFAX: (415) 368-0709
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 327 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
 ; INDIVIDUAL ISOLATE: region
 ;
 US-08-477-292-17

Query Match 98.3%; Score 1076; DB 3; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.4e-104;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVISANGEPTVKLYTSVENAQQDGKIALPHDIDGESRVVQDYDNQHEQDRPT 60
 Db 61 QLFYSPRVISANGEPTVKLYTSVENAQQDGKIALPHDIDGESRVVQDYDNQHEQDRPT 120
 Qy 61 PSPAPSRPFPVLRANDVLWLSLTAAFYDQSTGYSSTGPVYSDSVTLVNVATGQAQAVRS 120
 Db 121 PSPAPSRPFPVLRANDVLWLSLTAAFYDQSTGYSSTGPVYSDSVTLVNVATGQAQAVRS 180
 Qy 121 LDWTKVTLGRPLSTIQKXTEFFVPLRGRKLSPWEAGTKGPYNTNTASDQLLVEN 180
 Db 181 LDWTKVTLGRPLSTIQKXTEFFVPLRGRKLSPWEAGTKGPYNTNTASDQLLVEN 240
 Qy 181 AAGHRAVIASTYTTSLGAGPVSISAVAVLAP 210
 Db 241 AAGHRAVIASTYTTSLGAGPVSISAVAVLAP 270

RESULT 8 {
 US-07-870 (85)-15 Application US/07870985A
 / Sequence 15
 / Patent No 455492
 / GENERAL INFORMATION:
 / APPLICANT: Reyes, Gregory R.
 / APPLICANT: Bradley, Daniel W.
 / APPLICANT: Two, Jr., Shin
 / APPLICANT: Purdy, Michael A.
 / APPLICANT: Tam, Albert W.
 / APPLICANT: Krawczynski, Krzysztof Z.
 / TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 / NUMBER OF SEQUENCES: 22
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Denlinger & Associates
 / STREET: 350 Cambridge Avenue, Suite 250
 / CITY: Palo Alto
 / STATE: CA
 / ZIP: 94306
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/07/870,985A
 / FILING DATE: 20-APRIL-1992
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 822,335
 / FILING DATE: 17-JAN-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 505,888
 / FILING DATE: 05-APRIL-1990
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 426,921
 / FILING DATE: 13-OCTOBER-1989
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 336,672
 / FILING DATE: 16-JUNE-1989
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 316,1989
 / FILING DATE: 11-APRIL-1989
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 208,997
 / FILING DATE: 17-JUNE-1988
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Fabian, Gary R.
 / REGISTRATION NUMBER: 33,875
 / REFERENCE/DOCKET NUMBER: 4600-0293.41
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 324-0880
 / TELEX/FAX: (415) 324-0960
 / INFORMATION FOR SEQ ID NO: 15:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 327 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ORIGINAL SOURCE:
 / INDIVIDUAL ISOLATE: SG3, BURMA, FIGURE 9
 / US-07-870-985A-15

Query Match 98.3%; Score 1076; DB 4; Length 327;
 Best Local Similarity 100.0%; Prod. No. 4.4e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVISANGEPTVKLYTSVENAQQDGKIALPHDIDGESRVVQDYDNQHEQDRPT 60
 Db 61 QLFYSPRVISANGEPTVKLYTSVENAQQDGKIALPHDIDGESRVVQDYDNQHEQDRPT 120
 Qy 61 PSPAPSRPFPVLRANDVLWLSLTAAFYDQSTGYSSTGPVYSDSVTLVNVATGQAQAVRS 120
 Db 121 PSPAPSRPFPVLRANDVLWLSLTAAFYDQSTGYSSTGPVYSDSVTLVNVATGQAQAVRS 180
 Qy 121 LDWTKVTLGRPLSTIQKXTEFFVPLRGRKLSPWEAGTKGPYNTNTASDQLLVEN 180
 Db 181 LDWTKVTLGRPLSTIQKXTEFFVPLRGRKLSPWEAGTKGPYNTNTASDQLLVEN 240
 Qy 181 LDWTKVTLGRPLSTIQKXTEFFVPLRGRKLSPWEAGTKGPYNTNTASDQLLVEN 180
 Db 181 LDWTKVTLGRPLSTIQKXTEFFVPLRGRKLSPWEAGTKGPYNTNTASDQLLVEN 240
 Qy 181 AAGHRAVIASTYTTSLGAGPVSISAVAVLAP 210
 Db 241 AAGHRAVIASTYTTSLGAGPVSISAVAVLAP 270

RESULT 9 {
 PCT-US95-13703-17 Application PC/TUS9513703
 / Sequence 17
 / GENERAL INFORMATION:
 / APPLICANT:
 / TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
 / NUMBER OF SEQUENCES: 31
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Denlinger & Associates
 / STREET: P.O. Box 60850
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94306-0850
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: PCT/US95/13703
 / FILING DATE:
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Fabian, Gary R.
 / REGISTRATION NUMBER: 33,875
 / REFERENCE/DOCKET NUMBER: 4600-0293.41
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 324-0880
 / TELEX/FAX: (415) 324-0960
 / INFORMATION FOR SEQ ID NO: 17:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 327 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: protein
 / HYPOTHETICAL: NO
 / ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
 INDIVIDUAL ISOLATE: region
 PCT-US93-13703-17

Query Match 98.3%; Score 1076; DB 5; Length 327;
 Best Local Similarity 100.0%; Pred. No. 4.e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVVSAANGEPTVKLYTSVENAQQDKGIAIPHDIDGESRVIQDYDNQHEQDREPT 60
 Db 61 QLFYSPRVVSAANGEPTVKLYTSVENAQQDKGIAIPHDIDGESRVIQDYDNQHEQDREPT 120
 Qy 61 PSPAPSRPFSTLPRANDVWLSLTAEYDOSTGSSSTGPVYVSDSVTLVNATGAQAYARS 120
 Db 121 PSPAPSRPFSTLPRANDVWLSLTAEYDOSTGSSSTGPVYVSDSVTLVNATGAQAYARS 180
 Qy 121 LDWTKVTLDRPLSTIQYSKTFVVLPLRGKLSFWEAGTTKAGYPNNNTASDQLIVEN 180
 Db 181 LDWTKVTLDRPLSTIQYSKTFVVLPLRGKLSFWEAGTTKAGYPNNNTASDQLIVEN 240
 Qy 181 AAGHRAISTYTTSLGAGPVYSISAVAVLAP 210
 Db 241 AAGHRAISTYTTSLGAGPVYSISAVAVLAP 270

RESULT 10
 Sequence (17) Application US/08259148A
 Patent No. 741190

GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R.
 APPLICANT: Bradley, Daniel W.
 APPLICANT: Twu, Jr-Shin
 APPLICANT: Purdy, Michael A.
 APPLICANT: Tam, Albert W.
 APPLICANT: Krawczynski, Krzysztof Z.
 APPLICANT: Yarbough, Patrice D.

TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/259,148A
 FILING DATE: 13-JUN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 822,335
 FILING DATE: 17-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 505,888
 FILING DATE: 05-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 420,921
 FILING DATE: 13-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 367,486
 FILING DATE: 16-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 336,672
 FILING DATE: 11-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 208,997
 FILING DATE: 17-JUN-1988

ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 9
 US-08-259-148A-17

Query Match 98.3%; Score 1076; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 6.7e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVVSAANGEPTVKLYTSVENAQQDKGIAIPHDIDGESRVIQDYDNQHEQDREPT 60
 Db 170 QLFYSPRVVSAANGEPTVKLYTSVENAQQDKGIAIPHDIDGESRVIQDYDNQHEQDREPT 229

Qy 61 PSPAPSRPFSTLPRANDVWLSLTAEYDOSTGSSSTGPVYVSDSVTLVNATGAQAYARS 120
 Db 230 PSPAPSRPFSTLPRANDVWLSLTAEYDOSTGSSSTGPVYVSDSVTLVNATGAQAYARS 289

Qy 121 LDWTKVTLDRPLSTIQYSKTFVVLPLRGKLSFWEAGTTKAGYPNNNTASDQLIVEN 180
 Db 290 LDWTKVTLDRPLSTIQYSKTFVVLPLRGKLSFWEAGTTKAGYPNNNTASDQLIVEN 349

Qy 181 AAGHRAISTYTTSLGAGPVYSISAVAVLAP 210
 Db 350 AAGHRAISTYTTSLGAGPVYSISAVAVLAP 379

RESULT 11
 Sequence (17) Application US/08484054
 Patent No. 570689

GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R.
 APPLICANT: Bradley, Daniel W.
 APPLICANT: Twu, Jr-Shin
 APPLICANT: Purdy, Michael A.
 APPLICANT: Tam, Albert W.
 APPLICANT: Krawczynski, Krzysztof Z.
 TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/259,148A
 FILING DATE: 13-JUN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 822,335
 FILING DATE: 17-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 505,888
 FILING DATE: 05-APR-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 420,921
 FILING DATE: 13-OCT-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 367,486
 FILING DATE: 16-JUN-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 336,672
 FILING DATE: 11-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 208,997
 FILING DATE: 17-JUN-1988

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,054
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 870,985
 FILING DATE: 20-APR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 822,335

PRIORITY INFORMATION:
 FILING DATE: 17-JAN-1992
 APPLICATION NUMBER: US 505,888
 FILING DATE: 05-APRIL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 420,921
 FILING DATE: 13-OCTOBER-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 367,486
 FILING DATE: 16-JUNE-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 336,672
 FILING DATE: 11-APRIL-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 208,997
 FILING DATE: 17-JUNE-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Sholtz, Charles K.
 REGISTRATION NUMBER: 38,615
 REFERENCE/DOCKET NUMBER: 4600-0093.38
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 9
 US-08-484-054-17

Query Match 98.3%; Score 1076; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 6.7e-104;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QLFYSPRVVSAANGPPTVKLYTSVNAQQDQKGIAIPHDIDGESRVVIQDYDNQHEQDRPT 60
 Db 170 QLFYSPRVVSAANGPPTVKLYTSVNAQQDQKGIAIPHDIDGESRVVIQDYDNQHEQDRPT 229

Qy 61 PSPAPSRRPSVLRANDVLMISLTAEYDOSTYGSSTGPyVSDSVTLNVATGAQAVARS 120
 Db 230 PSPAPSRRPSVLRANDVLMISLTAEYDOSTYGSSTGPyVSDSVTLNVATGAQAVARS 289

Qy 121 LDWTKVTLDRPLSTIQYSKTPFVLPLRGKLSFWEAHTTKAGYPYNTNTASDQLLVEN 180
 Db 290 LDWTKVTLDRPLSTIQYSKTPFVLPLRGKLSFWEAHTTKAGYPYNTNTASDQLLVEN 349

Qy 181 AAGHRVAISTYTTSLGAGPVYSISAVAVLAP 210
 Db 350 AAGHRVAISTYTTSLGAGPVYSISAVAVLAP 379

RESULT 12
 US-07-876-941-17
 Sequence 17 Application US/07876941A
 Patent No. 588528
 GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R.
 APPLICANT: Bradley, Daniel W.
 APPLICANT: Tam, Albert W.
 APPLICANT: Mitchell, Carl
 TITLE OF INVENTION: Hepatitis B Virus Peptide Antigen and
 TITLE OF INVENTION: Antibodies
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Denlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA

RESULT 13
 US-07-870-9852-17
 Sequence 17 Application US/07870985A
 Patent No. 6455392
 GENERAL INFORMATION:
 APPLICANT: Reyes, Gregory R.

APPLICANT: Bradley, Daniel W.
 APPLICANT: Twu, Jr-Shin
 APPLICANT: Purdy, Michael A.
 APPLICANT: Tam, Albert W.
 APPLICANT: Krawczynski, Krzysztof Z.
 TITLE OF INVENTION: Hepatitis E Virus Vaccine and Method
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Dehlinger & Associates
 STREET: 350 Cambridge Avenue, Suite 250
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94306
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/870,985A
 FILING DATE: 20-APRIL-1992
 CLASSIFICATION: 435
 APPLICATION NUMBER: US 822,335
 FILING DATE: 17-JAN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 367,486
 FILING DATE: 16-JUNE-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 505,888
 FILING DATE: 05-APRIL-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 420,921
 FILING DATE: 13-OCTOBER-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 336,672
 FILING DATE: 11-APRIL-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 208,997
 FILING DATE: 17-JUNE-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fabian, Gary R.
 REGISTRATION NUMBER: 33,875
 REFERENCE/DOCKET NUMBER: 4600-0093-3.0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 436 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: C2, BURMA, FIGURE 9
 US-07-870-985A-17

Query Match 98.3%; Score 1076; DB 4; Length 436;
 Best Local Similarity 100.0%; Pred. No. 6.e-104; Indels 0; Gaps 0;
 Matches 210; Conservative 0; Mismatches 0;

Qy 1 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 60
 Db 170 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 229
 Qy 61 PSPAPSRRPSVLRANDVWLSTAAEYDOSTYGGSTGPPVYSDSVTLVNATGAQAVARS 120
 Db 230 PSPAPSRRPSVLRANDVWLSTAAEYDOSTYGGSTGPPVYSDSVTLVNATGAQAVARS 289
 Qy 121 LDWTKVLDGRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGPYNTNTASDQLVEN 180
 Db 403 LDWTKVLDGRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGPYNTNTASDQLVEN 462

RESULT 14
 US-08-542-634-27
 ; Sequence 27, Application US/08542634
 ; Patent No. 6214970
 ; GENERAL INFORMATION:
 ; APPLICANT: Fuecht, Thomas R.
 ; APPLICANT: McAfee, C. Patrick O.
 ; APPLICANT: Varnough, Patrice O.
 ; APPLICANT: Zhang, Yifan
 ; TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Ave., Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94106
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/542,634
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 4600-0293-30
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 525 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: Single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)
 ; INDIVIDUAL ISOLATE: r62kDa, 56.5 kDa
 ; US-08-542-634-27

Query Match 98.3%; Score 1076; DB 3; Length 525;
 Best Local Similarity 100.0%; Pred. No. 8.e-104; Indels 0; Gaps 0;
 Matches 210; Conservative 0; Mismatches 0;

Qy 1 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 60
 Db 283 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 342
 Qy 61 PSPAPSRRPSVLRANDVWLSTAAEYDOSTYGGSTGPPVYSDSVTLVNATGAQAVARS 120
 Db 343 PSPAPSRRPSVLRANDVWLSTAAEYDOSTYGGSTGPPVYSDSVTLVNATGAQAVARS 402
 Qy 121 LDWTKVLDGRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGPYNTNTASDQLVEN 180
 Db 403 LDWTKVLDGRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGPYNTNTASDQLVEN 462

Query Match 98.3%; Score 1076; DB 4; Length 436;
 Best Local Similarity 100.0%; Pred. No. 6.e-104; Indels 0; Gaps 0;
 Matches 210; Conservative 0; Mismatches 0;

Qy 1 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 60
 Db 170 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 229
 Qy 61 PSPAPSRRPSVLRANDVWLSTAAEYDOSTYGGSTGPPVYSDSVTLVNATGAQAVARS 120
 Db 230 PSPAPSRRPSVLRANDVWLSTAAEYDOSTYGGSTGPPVYSDSVTLVNATGAQAVARS 289
 Qy 121 LDWTKVLDGRPLSTIQYSKTFVPLRGKLSFWEAGTTKAGPYNTNTASDQLVEN 180
 Db 463 QLFYSPRVVANGEPTVLYTSEVNAQDKGIAIPHDIDLGESERVVTDYDNQHEQDRT 492

RESULT 15
PCT-US95-13703-27
Sequence 27 Application PC/TUSS9513703
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT-US95/13703
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0293 .41
TELECOMMUNICATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)
INDIVIDUAL ISOLATE: r62kDa, 56.5 kDa
PCT-US95-13703-27

Query Match 98.3%; Score 1076; DB 5; Length 525;
Best Local Similarity 100.0%; Pred. No. 8.0e-104;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	Db	Start	End	Sequence
Qy 1	Db 283	1	61	QLFYSRPVNSANGEPTVCLYTSVENAQDKGIAAPHDIDGESRVVIQDYDNQHEQDPT
Qy 61	Db 343	61	121	PSPABSRPFSLVRANDVLWLSLTAAEYDOSTYGSSTGPVYVSDSLTVNATGAQAVARS
Qy 121	Db 403	121	181	LDWTKVTLDRPLSTIQYSKTFVFLPLRGKLSFWEAQTTKAGYPNTNTASDQLLVEN
Qy 181	Db 463	181	210	AAGHRVAISYTTSILGAPSISAVAVLAP
Qy 210	Db 342	210	462	463 AAGHRVAISYTTSILGAPSISAVAVLAP

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Scoring table:	BLOSUM62					
Searched:	Gapop 10.0 , Gapext 0.5					
Total number of hits satisfying chosen parameters:	141681					
Minimum DB seq length: 0						
Maximum DB seq length: 200000000						
Post-processing: Minimum Match 0%						
Post-processing: Maximum Match 100%						
Database :	SwissProt_42;*					
		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
		SUMMARIES				
Result No.	Score	Query	Match	Length	DB ID	Description
1	1076	98.3	660	1	VST2_HEVBU	P29126 hepatitis e
2	1076	98.3	660	1	VST2_HEVPA	P33426 hepatitis e
3	1060	96.8	485	1	VST2_HEVRM	P00270 hepatitis e
4	1060	96.8	660	1	VST2_HEVME	Q04611 hepatitis e
5	1043	95.3	659	1	VST2_HEVME	Q0350 hepatitis e
6	91.5	8.4	1305	1	F1SK_YERPE	Q82977 yersinia pe
7	90	8.2	1045	1	GUNB_CELF1	P26725 cellulomona
8	89	8.1	477	1	KPYK_BORBU	051122 borrelia bu
9	89	8.1	1802	1	HKK1_YEAST	P41809 saccharomyces
10	84.5	7.7	431	1	EURA_ECOLI	P12283 escherichia
11	84.5	7.7	431	1	PURA_SALTY	Q8xgp1 salmonella
12	84	7.7	432	1	ENO_BIFOLIO	Q89519 bifidobacterium
13	83	7.6	617	1	FXK1_MOUSE	P42128 mus musculus
14	83	7.6	765	1	EGIX_ECOLI	P33363 escherichia
15	82.5	7.5	234	1	EPDN_RHDV3	P27411 rabbit hemo
16	82.5	7.5	278	1	ETUJ_ECOLI	P777277 escherichia
17	82	7.5	335	1	GCAB_MOUSE	P01864 mus musculus
18	81.5	7.4	2344	1	POLN_RHDM	P27410 rabbit hemo
19	81.5	7.4	3354	1	CADN_HUMAN	Q9n251 homo sapien
20	81	7.4	418	1	EFPTU_CHLRE	P17746 chlamydomon
21	81	7.4	563	1	GUNB_CLOTRM	P04536 clostridium
22	80.5	7.4	799	1	AFSK_STRCO	P54741 streptomyces
23	79.5	7.3	279	1	ETUJ_SALTY	P41794 salmonella
24	79.5	7.3	1020	1	CARY_JACPL	Q9r189 lactobacillus
25	79	7.2	541	1	YD18_MYCTU	Q10531 mycobacterium
26	78.5	7.2	335	1	ISH1_MYCTU	Q53458 mycobacterium
27	78.5	7.2	584	1	PHAC_BORPE	P35077 bordetella
28	78.5	7.2	1256	1	ATL_STRAU	P52081 staphylococcus
29	78	7.1	569	1	YICH_ECOLI	P31433 escherichia
30	78	7.1	983	1	Y144_HUMAN	Q14157 homo sapien
31	78	7.1	1077	1	E22K3_CAEEL	Q19172 caenorhabditis
32	77	7.0	308	1	XERD_BIEFLO	Q72892 bifidobacterium
33	77	7.0	433	1	KCG3_RAT	Q8rs23 rattus norvegicus

RESULT 2						
Db	514	LDWTKVTLGRPLSTIQNSKTFPLRLGKLSFWEAGTTKAGPYNNNTASDQILVEN	573	574	AAGHRAISTYTTSGAGPYTSIAYAVLAP	603
Qy	181	AAGHRAISTYTTSGAGPYTSIAYAVLAP	210			
Db						
Qy	181	AAGHRAISTYTTSGAGPYTSIAYAVLAP	210			
Db						
Qy	574	AAGHRAISTYTTSGAGPYTSIAYAVLAP	603			
Db						
RESULT 3						
Db	VST2	HEVPA	STANDARD;	PRT;	660 AA.	
	ID	VST2	HEVPA			
	AC	P33426;				
	DT	01-FEB-1994	(Rel. 28, Created)			
	DT	01-FEB-1994	(Rel. 28, Last sequence update)			
	DI	01-FEB-1994	(Rel. 28, Last annotation update)			
	DE	Structural protein 2 precursor (ORF2).				
	OS	Hepatitis E virus (strain Pakistan) (HEV).				
	OC	Viruses; ssRNA positive-strand viruses, no DNA stage;				
	OC	Hepatitis E-like viruses.				
	NCBI_TAXID	33774				
	RN					
	RP					
	RX					
	RA					
	RA	Tearev S.A., Emerson S.U., Reyes G.R., Tsareva T.S., Legters L.J.,				
	RA	Malik I.A., Iqbal M., Purcell R.H.,				
	RA	"Characterization of a Prototype strain of hepatitis E virus."				
	RT	Proc. Natl. Acad. Sci. U. S. A. 89:559-563(1992).				
	RL	- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING				
	CC	THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA				
	CC	BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.				
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	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
	CC	the European Bioinformatics Institute. There are no restrictions on its				
	CC	use by non-profit institutions as long as its content is in no way				
	CC	modified and this statement is not removed. Usage by and for commercial				
	CC	purposes requires a license agreement (see http://www.isb-sib.ch/) or send an email to license@isb-sib.ch.				
	CC	CC BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.				
	DR	M80581;	AAA45727.1;			
	DR	InterPro:	IPR004261;	SP2.		
	DR	InterPro:	IPR008975;	Viral_cap_coat.		
	DR	PFAM:	PF03014;	SP2;	1.	
	DR	KW				
	FT	SIGNAL.	1	22	BY SIMILARITY.	
	FT	CHAIN	23	660	STRUCTURAL PROTEIN 2.	
	SQ	SEQUENCE	660 AA;	70980 MW;	8093BC53CB46FD3 CRC64;	
	Query Match	98 %	Score 1076;	DB 1,	Lenth 660;	
	Best Local Similarity	100.0%	Pred. No. 6.2e-86;			
	Matches 210;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0	
Qy	1	QLFYSPRVVSANGEPTVKLYTSVENAQDKGIAPIHDIDLGESRVVIQDYDNOHQDRPT	60			
Db	394	QLFYSPRVVSANGEPTVKLYTSVENAQDKGIAPIHDIDLGESRVVIQDYDNOHQDRPT	453			
Qy	61	PSPASPRPFSVLRANDVLMISITAEXYDOSTYGSSTCPVYSDSITLVNVATGAQAYARS	120			
Db	454	PSPASPRPFSVLRANDVLMISITAEXDOSTYGSSTCPVYSDSITLVNVATGAQAYARS	513			
Qy	121	LDWTKVTLGRPLSTIQYSKTFVPLRLGKLSFWEAGTTKAGPYNNNTASDQILVEN	180			
Db	514	LDWTKVTLGRPLSTIQYSKTFVPLRLGKLSFWEAGTTKAGPYNNNTASDQILVEN	573			
Qy	181	AAGHRAISTYTTSGAGPYTSIAYAVLAP	210			
Db	574	AAGHRAISTYTTSGAGPYTSIAYAVLAP	603			

Page 3

RESULT 5					
	VST2	HEVME	STANDARD;	PRT;	659 AA.
Qy	ID VST2	HEVME			
AC Q03550;					
DT 01-Oct-1993	(Rel. 27, Created)				
DT 01-Oct-1993	(Rel. 27, Last sequence update)				
DT 01-Feb-1994	(Rel. 28, Last annotation update)				
DB Structural protein 2 precursor.					
DR Hepatitis B virus (strain Mexico) (HEV).					
OS Viruses; ssRNA positive-strand viruses, no DNA stage;					
OC Hepatitis B-like viruses.					
OX NCBI_TAXID=31768;					
RN					
RP SEQUENCE FROM N.A.					
RX MEDLINE=93079857; PubMed=1448913;					
RA Huang C.C., Nguyen D., Fernandez J., Yun K.Y., Fry K.E.,					
RA Bradley D.W., Tam A.W., Reyes G.R.;					
RA "Molecular cloning and sequencing of the Mexico isolate of hepatitis E virus (HEV).";					
RL Virology 191: 550-558 (1992).					
- FUNCTION: CONTAINS A HIGH BASIC AMINO ACID CONTENT SUGGESTING THAT IT MAY BE INVOLVED IN THE ENCAPSIDATION OF THE GENOMIC RNA BY EFFECTIVELY NEUTRALIZING THE NEGATIVELY CHARGED RNA.					
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CC	EMBL; M74506; AAU45732; 1;	-.
DR	PRIB; B44212; B44212.	
DR	InterPro; IPR04261; SP2.	
DR	InterPro; IPR08975; Viral_cap_coat.	
DR	Pfam; PF03014; SF2; 1.	
KW	SIGNAL	22
FT	CHAIN	1
SQ	SEQUENCE	659 AA; 70640 MW; CF75E75EFDFBE2C CRC64;
	BY SIMILARITY.	
Query Match	95.3%; Score 1043; DB 1; Length 659;	
Best Local Similarity	94.3%; Pred. No. 4.6e-83;	
Matches	198; Conservative 9; Mismatches 3; Indels 0; Gaps 0;	
Qy	1 QLPYSPVVSANGSPVTKLYTSVNAQODKGTAIPHDLDGSRVIVDQYDNQHEQDRAFT 60	
Db	393 QLPYSPVVSANGSPVTKLYTSVNAQODKGTAIPHDLDGSRVIVDQYDNQHEQDRAFT 452	
Qy	61 PSPAPSPRFPSVLANDVILWLSLTAAEYDQSTGSSSTGPVYVSDSVTLVNATGAQAVARS 120	
Db	453 PSPAPSPRFPSVLANDVILWLSLTAAEYDQSTGSSSTGPVYVSDSVTLVNATGAQAVARS 512	
Qy	121 LDWTKVTLGDRPLSTIQYSKTPFVPLRGKLSFWEAFTTKAGXPYNNNTTASDQLIVEN 180	
Db	513 LDWSKVTLGDRPLTPEQYSKTPFVPLRGKLSFWEAFTTKAGXPYNNNTTASDQLIVEN 572	
Qy	181 AAGHRVALSTYTTSLGAGPVTISAVAVIAP 210	
Db	573 AAGHRVALSTYTTSLGAGPVTISAVAVIAP 602	
	RESULT 6	
	FTSK_YEPB	
ID	FTSK_YERPE	STANDARD;
AC	Q8ZGC7;	PRY; 1305 AA.
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	DNA translocase ftsk.	
GN	FTSK OR YPO1376 OR Y2800.	
OS	Yersinia pestis.	
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	
OC	Enterobacteriaceae; Yersinia.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CO-92 / Biovar Orientalis;	
RX	MSDBLINKS=21470413; Published=1586360;	
RA	Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,	
RA	Prentice M.B., Seabinia M., James K.D., Churcher C., Mungall K.L.,	
RA	Baker S., Basham D., Bentley S.D., Brooks K., Cardeno-Tarraga A.M.,	
RA	Chillingworth T., Cronin A., Davies P.M., Davis P.J., Dougan G.,	
RA	Feltwell T., Hamlin N., Holroyd S., Jageel S., Karlyshev A.V.,	
RA	Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,	
RA	Simmonds M., Skeletal J., Stevens K., Whitehead S., Barrell B.G.;	
RA	"Genome sequence of Yersinia pestis, the causative agent of plague.";	
RL	Nature 413:523-527(2001).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=KIM5 / Biovar Mediavallis;	
RX	MSDBLINKS=22137863; PubMed=12142230;	
RA	Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Libes P.,	
RA	Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,	
RA	Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,	
RA	Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,	
RA	Perry R.D.;	
RT	"Genome sequence of Yersinia pestis KIM."	
J. Bacteriol. 184:4601-4611(2002).		
RL	-.- FUNCTION: DNA motor protein, which is both required to move DNA	
CC	out of the region of the septum during cell division and for the	
CC	septum formation. Tracks DNA in an ATP-dependent manner by	
CC	generating positive supercoils in front of it and negative	

supercoils behind it. Also plays a role in resolution of dimer chromosomes by regulating the xerC and xerD recombination complex, possibly by switching the catalytic state of the two recombinases required for the targeting of FtsQ, FtsL and FtsI to the septum (By similarity).

SUBUNIT: Homohexamer. This suggests the formation of a ring between the two cells at the septum that surrounds DNA (By similarity).

-1- SUBCELLULAR LOCATION: Integral membrane protein. Located at the septum. The large C-terminal part of the protein is cytoplasmic (Potential).

-1- SIMILARITY: Contains 1 PtkA domain.

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C	EMBL; AJ41148; CAC90405.1;	-	
R	AAMB8350.1;	-	
R	AB011883; AAMB8350.1;	-	
R	AB168;	-	
R	AB168;	-	
R	HAMAP; MF_01809;	- ; 1.	
R	INTERPRO; IPR002543;	FtsK_SPOIIIE.	
R	PF01880;	FtsK_SPOIIIE.	
R	PROSITE; PS50901; FTSK_1.		
W	Chromosome partition; Cell division; ATP-binding; DNA-binding;		
W	Transmembrane.		
T	TRANSMEM	22	POTENTIAL.
T	TRANSMEM	76	POTENTIAL.
T	TRANSMEM	111	POTENTIAL.
T	TRANSMEM	153	POTENTIAL.
T	TRANSMEM	180	POTENTIAL.
T	DOMAIN	949	POTENTIAL.
T	PB BIND	966	FtsK.
O	SPOIIE_NCR	1305 AA:	ATP (POTENTIAL).
O		140681 MW:	D25C95954.F1839 CRC44;

Query Match	8.4%;	Score 91.5;	DB 1;	Length 1305;
Best Local Similarity	27.9%;	Pred. No. 6.6;		
Matches	38;	Conservative	17; Mismatches 40;	Indels 41; Gaps
14	EPTVKLTVTSVENAQADKGIAHPHDIDLGESRVRVITDYNQHBEQDDEPTPSP-----			
	: :	: :	: :	: :
664	EPIPFETLSPVDTEDVDEPVQE-----	GKREBLLDDYDPEQ-----	VPTYQPVQQAHLGQS	
	: :	: :	: :	: :
64	APSRPFSVLRLNDVFLWLSLTAAEYDOSTYGST-----	-GPVYVSDSVTLVNVATGAOVAR		
	: :	: :	: :	: :
715	AFTOP-----	SHTQSTCQSTYQSTQSTPAFVSQP-----	VVTNSAIST	
	: :	: :	: :	: :

Micrococcineae; Cellulomonadaceae; Cellulomonas.
[1]
NCBI_TaxID=1708;
SEQUENCE_N_A.
MEDLINE:91100298; PubMed=19877122;

RA Meinke A., Braun C., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A.J.;
 RA "Unusual sequence organization in CenB, an inverting endoglucanase from Cellulomonas fimi.";
 RT J. Bacteriol. 173:308-314 (1991).
 RL [2]
 RN
 RP DOMAINS.
 RX MEDLINE=92041609; PubMed=1938913;
 MEINKE A., Gilkes N.R., Kilburn D.G., Miller R.C. Jr., Warren R.A. RA "Multiple domains in endoglucanase B (CenB) from Cellulomonas fimi: functions and relatedness to domains in other polypeptides.";
 J. Bacteriol. 173:7126-7135 (1991).
 RL -
 CC -1- FUNCTION: The biological conversion of cellulose to glucose generally requires three types of hydrolytic enzymes: (1) Endoglucanases which cut internal beta-1,4-glucosidic bonds; (2) Exocellulohydrolases that cut the disaccharide cellobiose from the nonreducing end of the cellulose polymer chain; (3) Beta-1,4-glucosidases which hydrolyze the cellobiose and other short cellooligosaccharides to glucose.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -1- MISCELLANEOUS: The linker region (also termed "hinge") may be a potential site for proteolytic cleavage.
 CC -1- MISCELLANEOUS: MAY CONTAIN A SECOND CBD IN THE CATALYTIC DOMAIN.
 CC -1- SIMILARITY: Contains 3 fibronectin type III domains.
 CC -1- SIMILARITY: Belongs to cellulase family E (family 9 of glycosidases).
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 CC -1- or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M64644; PAA23086.1; -.
 DR PIR; A39199; A39199.
 DR HSSP; P26221; 1TF4.
 DR InterPro; IPR01919; Bac_celose-bind.
 DR InterPro; IPR01956; CBD_3.
 DR InterPro; IPR008965; Cellobind.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR001701; Glyco_hydro_9.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 PFam; PF00053; CBM_3; 1.
 DR Pfam; PF00042; CBM_3; 1.
 DR Pfam; PF00041; Fn3; 3.
 DR Pfam; PF00759; Glyco_hydro_9; 1.
 SMART; SM00637; CBD_II; 1.
 SMART; SM00060; Fn3_-3.
 PROSITE; PS000592; GLYCOSTYL_HYDROL_F9_1.
 DR PROSITE; PS000698; GLYCOSTYL_HYDROL_F9_2; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Repeat; Signal.
 FT SIGNAL 1 33
 CHAIN 34 1045
 DOMAIN 34 643
 DOMAIN 644 650
 FT DOMAIN 651 733
 FT DOMAIN 734 748
 FT DOMAIN 749 830
 FT DOMAIN 831 846
 FT DOMAIN 847 930
 FT DOMAIN 931 944
 FT DOMAIN 945 1045
 FT ACT SITE 410 410
 FT ACT SITE 449 449
 FT ACT SITE 458 458
 FT DISULFIDE 946 1044
 SO SEQUENCEID 1045 AA; 108930 MW; AC2F7B94E3C4F0 CRC644;
 SO

Query Match 8.2%; Score 90; DB 1; Length 1045;
 Best Local Similarity 26.3%; Pred. No. 6.7;
 Matches 65; Conservative 18; Mismatches 100; Indels 64; Gaps 11;

DR PRINTS; PRO1050; PYRUVATKINASE.
 DR PRODOM; PD00109; Pyruvate_kinase; 1.
 DR TIGRFAMS; TIGR01064; Pyruv_kin; 1.
 DR PROSITE; PS00110; PYRUVATE_KINASE; 1.
 KW Pyruvate; Transferase; Kinase; Glycolysis; Magnesium;
 KW Complete proteome.

Qy 11 ANGEPITVKLYTSVENAQDQKGIAIPHDIDGESRVVQDY---DNOHQD---RPTPSP 63
 DR 544 AASDVTLSANYSBCCAQSGRGVSAAGTGLYVELSCVGQDTHPQQSOHREIQFRLT-GP 602
 FT ACT SITE 214 214 BY SIMILARITY.
 FT METAL 216 216 MAGNESIUM (BY SIMILARITY).
 FT METAL 237 237 MAGNESIUM (BY SIMILARITY).
 FT METAL 238 238 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 477 AA; 53032 MW; 40D3CCAC9ACB7D98 CRC64;

Query Match 8.1%; Score 89; DB 1; Length 477;
 Best Local Similarity 22.3%; Pred. No. 3;
 Matches 51; Conservative 35; Mismatches 74; Indels 70; Gaps 11;

Qy 8 VVSANGEPTVKLYTISVEN-----AQDKGIAIP-HDIDLGESRV- 45
 DR 200 IILTASGNPDVKLISKIENQEGIDNIEEAKASYGIMMVARQDMGYEVPAEDVPLAQLKLTQ 259
 Qy 46 -----VQDQTDNQH---EQDRDPTPSAPSREFSVRANNDVLSUITAAEYDQSTYGS 94
 DR 260 TCIXKGIPVITATQMLHTMIENPRTPRAEVSDIANAHLNGTDAIMLS-----GETAVGK 313
 Qy 95 STGPVYVSDSYLVNVATAQQAVALRSLDWT-----KVTLGRLPLSTI 136
 DR 314 -----YPIBAAVOM-MTISIAKKVEKHRTMTLYKDDELFDYDKSITRNYTKCAIDATKLMDI 366

RESULT 8
 KPYK BORRU STANDARD; PRT; 477 AA.
 ID HKRL YEAST
 AC P41809;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DB 367 ---KAIIIVDSLKCTKARTIMA-TYRASVPL-FLITINSERLARETALSFGV 410

SEQUENCE FROM N.A.
 STRAIN=ATCC 35210 / B31;
 MEDLINE=98065943; PubMed=9403685;
 Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 Dougherty B., Tomb J.-F., Fleischmann R., Richardson D., Richardson J.,
 Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.J.,
 Utterback T., Wathey L., McDonald L., Artiach P., Bowman C.,
 Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 Smith H.O., Venter J.C.;
 "Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.";
 RT RN TAXID=133;
 RN RP SEQUENCE FROM N.A.
 RX RA SEQUENCE FROM N.A.
 RA RA STRAIN=TNN 295;
 RA RA MEDLINE=94156857; PubMed=8113191;
 RA RA Kasahara S., Yamada H., Mio T., Shiratori Y., Miyamoto C.,
 RA RA Yabe T., Nakajima T., Ichishima E., Furuichi Y.;
 RT RT "Cloning of the Saccharomyces cerevisiae gene whose overexpression
 RT RT overcomes the effects of HM-1 killer toxin, which inhibits
 RT RT beta-glucan synthesis";
 RT RL J. Bacteriol. 176:1488-1499(1994).
 CC -!- FUNCTION: Could regulate beta-glucan synthesis. Overexpression
 CC -!- provides resistance to HM-1 killer toxin.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -!- Cloning of the Saccharomyces cerevisiae gene whose overexpression
 CC -!- overcomes the effects of HM-1 killer toxin, which inhibits
 CC -!- beta-glucan synthesis".
 CC -!- SIMILARITY: Belongs to the pyruvate kinase family.
 CC -!- CATALYTIC ACTIVITY: ATP + pyruvate = ADP + phosphoenolpyruvate.
 CC -!- COFACTOR: Requires magnesium and potassium.
 CC -!- PATHWAY: Glycolysis; Final step.
 CC -!- SUBUNIT: Homotrimer. (By similarity).
 CC -!- SIMILARITY: Belongs to the pyruvate kinase family.
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC -!- between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -!- or send an email to license@isb-sib.ch).
 CC -!- DR EMBL; S69101; AAB20051.1; -.
 CC -!- DR GerMonLine; 140912; -.
 CC -!- DR SGD; S0002828; HKR1.
 DR TIGR; BB0348; -.
 DR InterPro; IPR001697; Pyruvate_kinase.
 DR Pfam; PF00224; PK; 1.
 DR Pfam; PF02887; PK_C; 1.

KW Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 21 POTENTIAL; KILLER TOXIN-RESISTANT
 FT CHAIN 22 1802 HANSENULA MRKII KILLER TOXIN-RESISTANT PROTEIN 1.

FT TRANSMEM 1486 1506 SER/THR-RICH.
 FT DOMAIN 23 1478
 FT DOMAIN 453 788 12 X 28 AA TANDEM REPEATS OF S-[AV]-[P]-Y-T-S-S-P.
 FT REPEAT 453 480 1 (APPROXIMATE).
 FT REPEAT 481 508 2.
 FT REPEAT 509 536 3.
 FT REPEAT 537 564 4.
 FT REPEAT 565 592 5.
 FT REPEAT 593 620 6.
 FT REPEAT 621 648 7.
 FT REPEAT 649 676 8.
 FT REPEAT 677 704 9.
 FT REPEAT 705 732 10.
 FT REPEAT 733 760 11.
 FT REPEAT 761 788 12.
 FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1252 1252 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1293 1293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1342 1342 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1400 1400 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1802 AA; 188890 MW; E344CA6469785424 CRC64;

Query Match 8.1%; Score 89; DB 1; Length 1802;
 Best Local Similarity 26.3%; Pred. No. 17;
 Matches 44; Conservative 24; Mismatches 47; Indels 52; Gaps 8;

Qy 60 TPSPAPSPPSPVSLRNDVWLTSATAEYDQSTYGSSTGPVYVSDSVTLVNATGQAQAVR 119
 Db 1200 TPYSP-----NSYAWLP-TAIVVESERGPTTASNPNTGSPNPAIEPVAYVE 1249
 Qy 120 SLDPTKV-----LDGRPLASTICQSKNFFVFLPLRGKLSEWAGTTAGPYNN 168
 Db 1250 PINFLITIGFTAAINYVFLVQNPUSSAQ---IFNFNLVLK-----VPF 1291

Qy 169 NTTASDQLLVENAAAGHRVAISTYTSLGAG-----PVYSISAVYL 208
 Db 1292 SNTSSE---LDSNIGE---LSTFILSYRSQSSSTTSLSPKSISLSVV 1332

RESULT 10
 PURA_ECOLI
 ID PURA_ECOLI STANDARD PRT; 431 AA.
 AC P12283;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
 DE (AGSS) (AMPSase).
 GN PURA OR ADEK OR B41177 OR C5261 OR ECSS5153.
 OS Escherichia coli, O6, and
 Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC _ NCBI_TaxID=562, 217992, 83333;
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
 RP STRAIN=K12;
 RX MEDLINE=99066719; PubMed=3058695;
 RA Wolfe S.A., Smith J.M.;
 RT "Nucleotide sequence and analysis of the purA gene encoding
 adenylosuccinate synthetase of Escherichia coli K12.";
 RT "Evidence for an arginine residue at the substrate binding site of
 Escherichia coli adenylosuccinate synthetase as studied by chemical
 modification and site-directed mutagenesis.";
 RL J. Biol. Chem. 263:19147-19153 (1988).

RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=95334362; PubMed=7610040;

Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
 Blattner F.R.; "Analysis of the Escherichia coli genome VI: DNA sequence of the
 region from 92.8 through 100 minutes"; Nucleic Acids Res. 23:2105-2119(1995). [3]

RA RA
 RA RT
 RL RN
 RN SEQUENCE FROM N.A.
 RC STRAIN=06:HI / CPT073 / ATCC 700928;
 RX MEDLINE=22338234; PubMed=12471157;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rossch P.,
 RA Rakso D., Buckles E.L., Lioi S. R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";
 RT RT
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002). [4]

RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,
 RA Posfai G., Hackett J., Lirk S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RT RT
 RL Nature 409:529-533 (2001). [5]

RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / RIMD 0509952;
 RX MEDLINE=211516231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama T., Murata M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogawara N., Yasunaga T.,
 RA Kubara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
 RT RT
 RL DNA Res. 8:11-22 (2001). [6]

RN RN
 RP PARTIAL SEQUENCE OF 1-9.
 RC STRAIN=K12 / EMG2;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Link A.J., Robinson K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 RT Electrophoresis 18:1259-1313(1997). [7]

RN RN
 RP ACTIVE SITE LYS-140.
 RC MEDLINE=90202896; PubMed=2108156;
 RX MEDLINE=97443975; PubMed=9298646;
 RA Dong Q., Fromm H.J.;
 RT "Chemical modification of adenylosuccinate synthetase from Escherichia coli by pyridoxal 5'-phosphate. Identification of an active site lysyl residue";
 RT J. Biol. Chem. 265:6235-6240 (1990). [8]

RN RN
 RP SEQUENCE OF 145-147, AND MUTAGENESIS OF ARG-147.
 RX MEDLINE=91286237; PubMed=2061308;
 RA Dong Q., Liu F., Myers A.M., Fromm H.J.;
 RT "Site-directed mutagenesis of the phosphate-binding consensus sequence in Escherichia coli adenylosuccinate synthetase.";
 RT J. Biol. Chem. 266:12228-12233 (1991). [9]

RP RP
 RN MUTAGENESIS.
 RX MEDLINE=92129317; PubMed=1733940;
 RA Liu F., Dong Q., Fromm H.J.;
 RT "Site-directed mutagenesis of the phosphate-binding consensus sequence in Escherichia coli adenylosuccinate synthetase.";
 RT J. Biol. Chem. 267:2388-2392 (1992). [10]

RN RN
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISION TO 416.
 RX MEDLINE=96095802; PubMed=7490761;

RA Silva M.M., Poland B.W., Hoffman C.R., Fromm H.J., Honzatko R.B.;
 RT "Refined crystal structures of unligated adenylosuccinate synthetase
 from Escherichia coli.";
 RT J. Mol. Biol. 254:431-446 (1995).
 RL PDB; 1CG1; 17-JUN-99.
 RN DR PDB; 1CG0; 17-JUN-99.
 RP DR PDB; 1CG3; 17-JUN-99.
 RX DR PDB; 1CG4; 17-JUN-99.
 RA DR PDB; 1CH8; 29-DEC-99.
 RA DR PDB; 1CIB; 05-APR-00.
 RA DR PDB; 1KX9; 20-MAR-02.
 RA DR PDB; 1KXB; 20-MAR-02.
 RP DR PDB; 1KKF; 20-MAR-02.
 RX DR SWISS-2DPAGE; P12283; COLI.
 RA DR Ecogene; BG10790; purA.
 RA DR HAMAP; MF_00011; -;
 DR InterPro; IPR001114; Asucc_synthase.
 DR Pfam; PF00709; AdenyLsucc_synt; 1.
 DR Pfdom; PD001188; Asucc_synthase; 1.
 DR DR PDB; 00011; -;
 DR DR TIGREAMS; TIGR00184; purA; 1.
 DR DR PROSITE; PS00513; ADENYLOSUCCIN_SYN; 2;
 DR DR PROSITE; PS01266; ADENYLOSUCCIN_SYN; 1;
 DR DR Purine biosynthesis; Ligase; GTP-binding; Metal-binding; Magnesium;
 KW KW 3D-structure; Complete proteome.
 RN KW KW INIT_MET 0 0 G-V: SIGNIFICANT REDUCTION IN ACTIVITY.
 RP FT NP_BIND 12 18 GTP (POTENTIAL).
 RX FT ACT_SITE 140 140 PROBABLE.
 RA FT ACT_SITE 147 147 MAGNESIUM.
 RT FT METAL 13 13 MAGNESIUM. (VIA CARBONYL OXYGEN)
 RL FT METAL 40 40 MAGNESIUM.
 RN FT MUTAGEN 12 12 G-V: SIGNIFICANT REDUCTION IN ACTIVITY.

Query Match 7.7%; Score 84.5%; DB 1; Length 431;
 Best Local Similarity 24.3%; Prd. No. 6; 5; Gaps 11;
 Matches 51; Conservative 29; Mismatches 73; Indels 57; Gaps 11;

QY 28 QDGKIAIPHIDIGESRVVQDY---ONQHEODRTPS-----PAPSREFV---L 72
 Db 87 EDGIPVERRLLSEACPILDYHVALDNAREKGARGAKAIGTGRGIGPAYERKVARRL 146

QY 73 RANDVLWLSLTAAEYDQSTYGSSTGPVYVSDSUTLVNVATGQAVERSILDWTKTLDGRP 132
 Db 147 RVGDL-----FDKETFAEKLEKKEYNEHNQFLVNTYK----AEAVDYQKWLDDTMVA 192

QY 133 LSTI----OQYSKTFPVFL-PLRGKLFVWEAGTTKAGPY--NNNTTASDQ 175
 Db 193 VADILTSWVVDVSLLDQARQGDFFMFEAGAQGTLLDIDHT----YPVVTSSNTTAAAGG- 247

QY 176 LLVENAAGRVA----ISTYTTISGACP 199
 Db 248 VATSGGLGPRTYDYLGLIKAYSTRVGACP 277

RESULT 11

PURA_SALTY STANDARD; PRT; .431 AA.

ID PURA_SALTY QBXGF1; (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DR DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DR DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)
 DE (ADSS) (AMPBase).
 DE PURA OR STM366 OR STM4723 OR T4417.

GN OS Salmonella typhimurium, and
 OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Bacteroidales; Salmonella.

NCBI_TaxID=602, 601;

RP SEQUENCE FROM N.A.
 RC SPECIES-S.typhimurium; STRAIN=LIT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 Courtney L., Porwollik S., Ali J., Danté M., Du F., Hou S., Layman D.,
 Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

16-OCT-2001	(Rel. 40, Last annotation update)
DE	Periplasmic beta-D-glucosidase precursor (EC 3.2.1.21) (Gentibiose)
DE	(Cellulase) (Beta-D-glucoside glucohydrolase).
BGLX	OR B2132.
GN	Escherichia coli.
OC	Bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OS	Enterobacteriaceae; Escherichia.
OC	NCBI TaxID=562;
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=K12 / W3110;
RC	Yang M., Luoch S., Goddard A., Reilly D., Henzel W., Bass S.,
RL	Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RR	[2]
RN	SEQUENCE FROM N.A.
RP	STRAIN=K12 / BHB2600;
RC	Richertich P., Lakey N., Gryan G., Jaehn L., Mintz L., Robison K.,
RA	Church G.M.;
RA	Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
RR	[3]
RN	SEQUENCE FROM N.A.
RP	STRAIN=K12 / MG1655;
RC	MEDLINE=9726611; PubMed=978503;
RX	Blattner F.R., Plunkett G., III, Bloch C.A., Perri N.T., Burland V.
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA	Mau B., Shao Y.
RA	"The complete genome sequence of Escherichia coli K-12."
RL	Science 277:1453-1474 (1997).
RT	-- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-glucose residues with release of beta-D-glucose.
CC	-- SUBCELLULAR LOCATION: Periplasmic.
CC	-- SIMILARITY: Belongs to family 3 of glycosyl hydrolases.
CC	--
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CC	--
EMBL	U15049; AA38487.1; -.
EMBL	AE00007; AA60495.1; ALT_INIT.
EMBL	AE0000302; AAC75193.1; -.
PIR	C64981; C64981.
EcoGene	EGI12013; bg1X.
InterPro	IPR002772; Glyco_hydro_3C.
DR	InterPro; IPR001764; Glyco_hydro_3N.
DR	Pfam; PF00933; Glyco_hydro_3;
DR	Pfam; PF01915; Glyco_hydro_3_C; 1.
DR	PRINTS; PR00133; GLHYDROLASE3.
DR	PROSITE; PS00775; GLYCOSYL_HYDROL_F3; 1.
KW	Hydrolyase; Glycosidase; Periplasmic; signal; Complete proteome.
FT	SIGNAL 1 20 POTENTIAL.
FT	CHAIN 21 765 PERPLASMIC BETA-GLUCOSIDASE.
FT	ACT SITE 287 287 BY SIMILARITY.
SEQ	SEQUENCE 765 AA; 83460 MW; 0889BAE42B8F83 CRC64;
SQ	Query Match 7.6%; Score 83; DB 1; Length 765;
	Best Local Similarity 19.4%; Pred. No. 18;
	Matches 34; Mismatches 76; Indels 94; Gap
Qy	8 VVSGANGKVLTKTSVENVQQDKGIAIPHDIDLGESRVIQDYNHQEQ ---DRPT
Db	446 IKNAVGNGKVLYAKGANTVSDKGII-----DELNQYEAVKVDPPRS
Qy	64 APSRFESTVLRANDVILWLSLTAAEYDOSTGSSTGPVYVSDDSVTLVNATGAQAVARS
Db	491 MLDVAQTAQSDVV-----VAVVGEAQMAHEASRTDTITPQSORDLIA
Qy	124 T-----KYLDGRPLSTIQQYSKTCFVPLRGKLSFWEST-----

Db	541	TGKPLVLVLMGRPLALVKEDQADAI	--	LETFWAGTEGGNAIADVLFQDYNPSGK	594
Qy	160	--	--	-TKAGXPYN-----YNTTASDQILVENAA--	--GHRVAISTY 191
Db	595	LPMSPRSVGQ1PVYVSHLNTGRPYNAADKPNKYTSRYFDE	--	ANGALYPFGYGLSRTTF	651
Qy	192	TMSLGAGPVSISA 204			
Db	652	TVS--	--	DVKLSA 660	
RESULT 15					
	POIN_RHDV3	STANDARD;	PRT;	234 AA.	
	ID AC P27411;				
	DT 01-AUG-1992	(Rel. 23, Created)			
	DT 01-AUG-1992	(Rel. 23, Last sequence update)			
	DT 2002-2003	(Rel. 41, Last annotation update)			
	DE Non-structural polyprotein [Contains: Coat Protein] (Fragment).				
	OS Rabbit hemorrhagic disease virus (strain V-351) (RHDV).				
	OC ssRNA positive-strand viruses, no DNA stage; Caliciviridae;				
	OC Lagovirus.				
	OX NCBI_TaxID:11977;				
	RN [1]				
	RP SEQUENCE FROM N.A.				
	RX MEDLINE=92307403; PubMed=1497750;				
	RA Milton I.D., Vlasak R., Nowotny N., Rodak L., Carter M.J.;				
	RT "Genomic 3' terminal sequence comparison of three isolates of rabbit				
	RT haemorrhagic disease virus";				
	RL FEMS Microbiol. Lett. 72:37-42 (1992).				
CC	--	--	--	--	--
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CC	or send an email to license@isb-sib.ch).				
CC	--	--	--	--	--
DR	EMLB: C211535; CAA7633..1; -.				
DR	PTR: S22134; S22134.				
DR	InterPro: IPR040405; Calicici_coat.				
DR	PFam: PF009105; Calicici_coat_1.				
KW	Polyprotein; Coat protein.				
FT	NON_TER 1				
FT	DOMAIN ? 234 AA; 2377 MW; COAT PROTEIN.				
SQ	SEQUENCE 234 AA; B6618654E2BE05A CRC64;				
Query Match 7.5%; Score 82.5; DB 1; Length 234;					
Best Local Similarity 22.5%; Prod. No. 4.4; Mismatches 88; Indels 45; Gaps 8;					
Matches 47; Conservative 29; MisMatches 88; Indels 45; Gaps 8;					
Qy	6 RPVVSANGEPVTY-KLYTSVE-NAQDKGIA1PHDIDIGESRVVQDNYHQDRPPPS 62				
Db	44 QPTNSANGTPVY-KLYTSVE-NAQDKGIA1PHDIDIGESRVVQDNYHQDRPPPS 62				
Qy	63 PAPSRPFES-----VLRANDVWLNLTAAYDOSTYGSSTGPYVVDSDVTLVNVAT 112				
Db	104 TPALAVPGKNTPTIMFAVSVRRTGDN--NATAGSVNGTQYGRCSQPLPTVIGSLNN -- 157				
Qy	113 GAQWARSLDWTWVTKTIDGEPPLSTIQSKTFFYLPRGKLSFWMEAGTITKAGTPY--NYN 169				
Db	158 -----YSSALMPGQ-----FFWVQLTPASGFWEIGLSVDGYFYAGTGAS 196				
Qy	170 TTA2D--QLLVENVAGHRYVAISTYTTSLG 196				
Db	197 TTIDLTENIDVPRGVGPBPSSKSTLVENIG 225				